GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 7, 2005, 00:51:17 ; Search time 6317 Seconds
(without alignments)
10798.186 Million cell updates/sec

Title: US-09-836-544C-28
Perfect score: 1200
Sequence: 1 ggggtgcaaagaagagacag.....aaataaagtgacagatgacc 1200

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
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15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1182.6	98.5	1201	6	BD015201	BD015201 TLiSa cel
2	1182.6	98.5	1204	6	AR380482	AR380482 Sequence
3	1182.6	98.5	1204	6	AX697951	AX697951 Sequence
4	1182.6	98.5	1204	6	AX818155	AX818155 Sequence
5	1182.6	98.5	1204	8	HUMCD27A	M63928 Homo sapien
6	1182.6	98.5	1323	8	BC012160	BC012160 Homo sapi
7	1181	98.4	1204	6	CQ721686	CQ721686 Sequence
8	1181	98.4	1300	6	CQ869620	CQ869620 Sequence
9	1181	98.4	1323	6	CS119000	CS119000 Sequence
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12	505.6	42.1	524	6	AX778265	AX778265 Sequence
13	451.8	37.6	1585	9	MUSCD27A	L24495 Mus musculu
14	435.2	36.3	1602	9	BC095844	BC095844 Rattus no
15	426	35.5	172571	8	AC006064	AC006064 Homo sapi
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c 25	235.8	19.7	483	6	CQ070114	CQ070114 Sequence
c 26	235.8	19.7	483	6	CQ097846	CQ097846 Sequence
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c 31	235.8	19.7	483	6	CQ295823	CQ295823 Sequence
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c 36	234.4	19.5	455	6	CQ184470	CQ184470 Sequence
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c 38	234.4	19.5	455	6	CQ271024	CQ271024 Sequence
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44	197.4	16.4	309	6	CS118999	CS118999 Sequence
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ALIGNMENTS

RESULT 1
BD015201
LOCUS BD015201 1201 bp DNA linear PAT 27-AUG-2002
DEFINITION TLiSa cell surface antigen and CD27 cell surface antigen, and utilization thereof.
ACCESSION BD015201
VERSION BD015201.1 GI:22556008
KEYWORDS JP 2001157592-A/19.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Seed,B., Aruffo,A. and Amiot,M.
TITLE TLiSa cell surface antigen and CD27 cell surface antigen, and utilization thereof
JOURNAL Patent: JP 2001157592-A 19 12-JUN-2001;
THE GENERAL HOSPITAL CORP
COMMENT OS Homo sapiens (human)
PN JP 2001157592-A/19
PD 12-JUN-2001
PF 04-OCT-2000 JP 2000305557
PR 13-JUL-1990 US 553759
PI BRIAN SEED,ALEJANDRO ARUFFO,MARTIN AMIOT
PC C12N15/09,C07K14/725,G01N33/53,C12N15/00
CC TLiSa cell surface antigen and CD27 cell surface antigen, and
CC utilization
CC thereof
FH Key Location/Qualifiers
FT CDS (101). .(880).
FEATURES Location/Qualifiers
source 1. .1201
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 98.5%; Score 1182.6; DB 6; Length 1201;
Best Local Similarity 99.6%; Pred. No. 1.6e-271;
Matches 1196; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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Db       1201 C 1201
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RESULT 2
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DEFINITION Sequence 1027 from patent US 6607879.
ACCESSION AR380482
VERSION AR380482.1 GI:40088116
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1204)
AUTHORS Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.
TITLE Compositions for the detection of blood cell and immunological response gene expression
JOURNAL Patent: US 6607879-A 1027 19-AUG-2003;
Incyte Corporation; Palo Alto, CA
FEATURES Location/Qualifiers
source 1. .1204
/organism="unknown"
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ORIGIN

Query Match 98.5%; Score 1182.6; DB 6; Length 1204;
Best Local Similarity 99.6%; Pred. No. 1.6e-271;
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RESULT 3
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DEFINITION  Sequence 1 from Patent WO03009862.
ACCESSION   AX697951
VERSION     AX697951.1  GI:29499010
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lucas,J., Dialynas,D. and Briggs,K.
  TITLE     Agonists and antagonists of modumet for use in the treatment of
            metabolic disorders
  JOURNAL   Patent: WO 03009862-A 1 06-FEB-2003;
            GENSET SA (FR)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match           98.5%;  Score 1182.6;  DB 6;  Length 1204;
  Best Local Similarity  99.6%;  Pred. No. 1.6e-271;
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Qy        721 GGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAACAAAGGAGAAAGTCCTGTGGA 780
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Qy       1200 C 1200
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Db       1201 C 1201


RESULT 4
AX818155
LOCUS       AX818155               1204 bp    DNA     linear   PAT 10-DEC-2003
DEFINITION  Sequence 26 from Patent WO03068268.
ACCESSION   AX818155
VERSION     AX818155.1  GI:39723234
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ek,S., Borrebaeck,C.A. and Ehinger,M.
  TITLE     Treatment&comma; diagnosis and imaging of disease
  JOURNAL   Patent: WO 03068268-A 26 21-AUG-2003;
            BIOINVENT INTERNATIONAL AB (SE)
FEATURES             Location/Qualifiers
     source          1. .1204
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ORIGIN

  Query Match             98.5%;  Score 1182.6;  DB 6;  Length 1204;
  Best Local Similarity   99.6%;  Pred. No. 1.6e-271;
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Db        841 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGTAG 900

Qy        901 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 960
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Db       1081 GCAGGAGCCCAGCCAGCTGCGCCTGCGCTGCAGGAGGGCGGGGGGCTCTGGTTGTAAAACA 1140

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Qy       1200 C 1200
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Db       1201 C 1201


RESULT 5
HUMCD27A
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LOCUS       HUMCD27A                1204 bp    mRNA    linear   PRI 31-DEC-1994
DEFINITION  Homo sapiens T cell activation antigen (CD27) mRNA, complete cds.
ACCESSION   M63928
VERSION     M63928.1  GI:180084
KEYWORDS    T-cell activation antigen CD27.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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REFERENCE   1  (sites)
  AUTHORS   Camerini,D., Walz,G., Loenen,W.A., Borst,J. and Seed,B.
  TITLE     The T cell activation antigen CD27 is a member of the nerve growth
            factor/tumor necrosis factor receptor gene family
  JOURNAL   J. Immunol. 147 (9), 3165-3169 (1991)
   PUBMED   1655907
COMMENT     Original source text: Homo sapiens cDNA to mRNA.
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ORIGIN

  Query Match           98.5%;  Score 1182.6;  DB 8;  Length 1204;
  Best Local Similarity  99.6%;  Pred. No. 1.6e-271;
  Matches 1196;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          1 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60
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Db          1 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60

Qy         61 CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTG 120
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RESULT 6
BC012160
LOCUS       BC012160                1323 bp    mRNA    linear   PRI 29-JUN-2004
DEFINITION  Homo sapiens tumor necrosis factor receptor superfamily, member 7,
            mRNA (cDNA clone MGC:20393 IMAGE:4575359), complete cds.
ACCESSION   BC012160
VERSION     BC012160.1  GI:15082490
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1323)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
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Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

PUBMED 12477932

REFERENCE 2 (bases 1 to 1323)

AUTHORS Strausberg,R.

TITLE Direct Submission

JOURNAL Submitted (02-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov

COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 29 Row: h Column: 11
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.

FEATURES Location/Qualifiers

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ORIGIN

Query Match 98.5%; Score 1182.6; DB 8; Length 1323;
Best Local Similarity 99.6%; Pred. No. 1.6e-271;
Matches 1196; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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Qy          1 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60
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Db         98 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 157

Qy         61 CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTG 120
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Db        158 CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTG 217

Qy        121 GTGGCTGTGCGTTCTGGGGACCCTGGTGGGGCTCTCAGCTACTCCAGCCCCCAAGAGCTG 180
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Qy        181 CCCAGAGAGGCACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240
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Qy        241 ATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 300
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Db        338 ATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 397

Qy        301 GGGGGTCTCCTTCTCTCCTGACCACCACACCCGGCCCCACTGTGAGAGCTGTCGGCACTG 360
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Qy        361 TAACTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCCTGTCG 420
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Db        458 TAACTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCCTGTCG 517

Qy        421 CAATGGCTGGCAGTGCAGGGACAAGGAGTGCACCGAGTGTGATCCTCTTCCAAACCCTTC 480
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Db        518 CAATGGCTGGCAGTGCAGGGACAAGGAGTGCACCGAGTGTGATCCTCTTCCAAACCCTTC 577

Qy        481 GCTGACCGCTCGGTCGTCTCAGGCCCTGAGCCCACACCCTCAGCCCACCCACTTACCTTA 540
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Db        578 GCTGACCGCTCGGTCGTCTCAGGCCCTGAGCCCACACCCTCAGCCCACCCACTTACCTTA 637

Qy        541 TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAG 600
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Db        638 TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAG 697

Qy        601 GCAGCTGCCTGCCCGGACTCTCTCTACCCACTGGCCACCCCAAAGATCCCTGTGCAGCTC 660
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Qy        661 CGATTTTATTCGCATCCTTGTGATCTTCTCTGGAATGTTCCTTGTTTTCACCCTGGCCGG 720
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Qy        721 GGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAACAAAGGAGAAAGTCCTGTGGA 780
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Qy        781 GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAGCACCATCCCCAT 840
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Qy        841 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGTAG 900
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Db        938 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGTAG 997

Qy        901 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 960
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Db        998 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 1057
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Qy        961 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020
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Db       1058 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1117

Qy       1021 GAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGTGGAGAGTGGGAA 1080
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Db       1118 GAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGTGGAGAGTGGGAA 1177

Qy       1081 GCAGGAGCCCAGCCAGCTGCGCGCGCG-TGCAGGAGGGCGGGGGCTCTGGTTGTAAGGCA 1139
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Db       1178 GCAGGAGCCCAGCCAGCTGCGCCTGCGCTGCAGGAGGGCGGGGGCTCTGGTTGTAAAACA 1237

Qy       1140 CACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGACAGATGAC 1199
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Qy       1200 C 1200
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Db       1298 C 1298
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RESULT 7
CQ721686
LOCUS       CQ721686               1204 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 7620 from Patent WO02068579.
ACCESSION   CQ721686
VERSION     CQ721686.1  GI:42282543
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 7620 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES             Location/Qualifiers
     source          1. .1204
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                     /db_xref="taxon:9606"
ORIGIN

  Query Match             98.4%;  Score 1181;  DB 6;  Length 1204;
  Best Local Similarity   99.5%;  Pred. No. 3.8e-271;
  Matches 1195;  Conservative    0;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          1 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60
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Db          1 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60

Qy         61 CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTG 120
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Qy        241 ATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 300
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Qy        301 GGGGGTCTCCTTCTCTCCTGACCACCACACCCGGCCCCACTGTGAGAGCTGTCGGCACTG 360
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Qy        361 TAACTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCCTGTCG 420
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Db        361 TAACTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCCTGTCG 420

Qy        421 CAATGGCTGGCAGTGCAGGGACAAGGAGTGCACCGAGTGTGATCCTCTTCCAAACCCTTC 480
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Db        481 GCTGACCGCTCGGTCGTCTCAGGCCCTGAGCCCACACCCTCAGCCCACCCACTTACCTTA 540

Qy        541 TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAG 600
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Qy        661 CGATTTTATTCGCATCCTTGTGATCTTCTCTGGAATGTTCCTTGTTTTCACCCTGGCCGG 720
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Qy        721 GGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAACAAAGGAGAAAGTCCTGTGGA 780
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Qy        901 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 960
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Db        901 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 960

Qy        961 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020
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Db        961 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020

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Qy       1081 GCAGGAGCCCAGCCAGCTGCGCGCGCG-TGCAGGAGGGCGGGGGCTCTGGTTGTAAGGCA 1139
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Qy       1200 C 1200
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Db       1201 C 1201
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RESULT 8
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LOCUS       CQ869620               1300 bp    DNA     linear   PAT 13-SEP-2004
DEFINITION  Sequence 41 from Patent WO2004074320.
ACCESSION   CQ869620
VERSION     CQ869620.1  GI:51999481
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Morris,D.W., Morris,D.W. and Malandro,M.S.
  TITLE     Novel therapeutic targets in cancer
  JOURNAL   Patent: WO 2004074320-A 41 02-SEP-2004;
            Sagres Discovery, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1300
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ORIGIN

  Query Match             98.4%;  Score 1181;  DB 6;  Length 1300;
  Best Local Similarity   99.5%;  Pred. No. 3.8e-271;
  Matches 1195;  Conservative    0;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          1 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60
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Db         98 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 157

Qy         61 CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTG 120
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Db        158 CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTG 217

Qy        121 GTGGCTGTGCGTTCTGGGGACCCTGGTGGGGCTCTCAGCTACTCCAGCCCCCAAGAGCTG 180
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Qy        181 CCCAGAGAGGCACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240
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Db        278 CCCAGAGAGGCACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 337

Qy        241 ATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 300
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Db        338 ATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 397

Qy        301 GGGGGTCTCCTTCTCTCCTGACCACCACACCCGGCCCCACTGTGAGAGCTGTCGGCACTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 GGGGGTCTCCTTCTCTCCTGACCACCACACCCGGCCCCACTGTGAGAGCTGTCGGCACTG 457

Qy        361 TAACTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCCTGTCG 420
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Qy        421 CAATGGCTGGCAGTGCAGGGACAAGGAGTGCACCGAGTGTGATCCTCTTCCAAACCCTTC 480
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Qy        481 GCTGACCGCTCGGTCGTCTCAGGCCCTGAGCCCACACCCTCAGCCCACCCACTTACCTTA 540
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Qy        541 TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAG 600
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Qy        601 GCAGCTGCCTGCCCGGACTCTCTCTACCCACTGGCCACCCCAAAGATCCCTGTGCAGCTC 660
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Qy        721 GGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAACAAAGGAGAAAGTCCTGTGGA 780
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Qy        781 GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAGCACCATCCCCAT 840
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Qy        841 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGTAG 900
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        938 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGGAG 997

Qy        901 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        998 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 1057

Qy        961 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020
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Db       1058 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1117

Qy       1021 GAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGTGGAGAGTGGGAA 1080
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Db       1118 GAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGTGGAGAGTGGGAA 1177

Qy       1081 GCAGGAGCCCAGCCAGCTGCGCGCGCG-TGCAGGAGGGCGGGGGCTCTGGTTGTAAGGCA 1139
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Qy       1140 CACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGACAGATGAC 1199
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Db       1238 CACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGACAGATGAC 1297

Qy       1200 C 1200
              |
Db       1298 C 1298


RESULT 9
CS119000
LOCUS       CS119000                1323 bp    DNA     linear   PAT 08-JUL-2005
DEFINITION  Sequence 1047 from Patent WO2005054508.
ACCESSION   CS119000
VERSION     CS119000.1  GI:70666946
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Bertucci,F., Houlgatte,R., Birnbaum,D. and Debono,S.
  TITLE     Gene expression profiling of colon cancer by dna microarrays and
            correlation with survival and histoclinical parameters
  JOURNAL   Patent: WO 2005054508-A 1047 16-JUN-2005;
            Ipsogen (FR); Institut Paoli-Calmettes, Ipc (FR); Institut National
            de la Sante et de la Recherche Medicale (INSERM) (FR)
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                     /note="tumor necrosis factor receptor superfamily, member
                     7(TNFRSF7) gene."
ORIGIN

  Query Match             98.4%;  Score 1181;  DB 6;  Length 1323;
  Best Local Similarity   99.5%;  Pred. No. 3.8e-271;
  Matches 1195;  Conservative    0;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          1 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60
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Db         98 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 157

Qy         61 CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTG 120
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Qy        121 GTGGCTGTGCGTTCTGGGGACCCTGGTGGGGCTCTCAGCTACTCCAGCCCCCAAGAGCTG 180
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Qy       181 CCCAGAGAGGCACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240
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Qy       241 ATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 300
Db       338 ATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 397

Qy       301 GGGGGTCTCCTTCTCTCCTGACCACCACACCCGGCCCCACTGTGAGAGCTGTCGGCACTG 360
Db       398 GGGGGTCTCCTTCTCTCCTGACCACCACACCCGGCCCCACTGTGAGAGCTGTCGGCACTG 457

Qy       361 TAACTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCCTGTCG 420
Db       458 TAACTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCCTGTCG 517

Qy       421 CAATGGCTGGCAGTGCAGGGACAAGGAGTGCACCGAGTGTGATCCTCTTCCAAACCCTTC 480
Db       518 CAATGGCTGGCAGTGCAGGGACAAGGAGTGCACCGAGTGTGATCCTCTTCCAAACCCTTC 577

Qy       481 GCTGACCGCTCGGTCGTCTCAGGCCCTGAGCCCACACCCTCAGCCCACCCACTTACCTTA 540
Db       578 GCTGACCGCTCGGTCGTCTCAGGCCCTGAGCCCACACCCTCAGCCCACCCACTTACCTTA 637

Qy       541 TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAG 600
Db       638 TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAG 697

Qy       601 GCAGCTGCCTGCCCGGACTCTCTCTACCCACTGGCCACCCCAAAGATCCCTGTGCAGCTC 660
Db       698 GCAGCTGCCTGCCCGGACTCTCTCTACCCACTGGCCACCCCAAAGATCCCTGTGCAGCTC 757

Qy       661 CGATTTTATTCGCATCCTTGTGATCTTCTCTGGAATGTTCCTTGTTTTCACCCTGGCCGG 720
Db       758 CGATTTTATTCGCATCCTTGTGATCTTCTCTGGAATGTTCCTTGTTTTCACCCTGGCCGG 817

Qy       721 GGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAACAAAGGAGAAAGTCCTGTGGA 780
Db       818 GGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAACAAAGGAGAAAGTCCTGTGGA 877

Qy       781 GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAGCACCATCCCCAT 840
Db       878 GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAGCACCATCCCCAT 937

Qy       841 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGTAG 900
Db       938 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGGAG 997

Qy       901 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 960
Db       998 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 1057

Qy       961 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020
Db      1058 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1117

Qy      1021 GAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGTGGAGAGTGGGAA 1080
Db      1118 GAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGTGGAGAGTGGGAA 1177

Qy      1081 GCAGGAGCCCAGCCAGCTGCGCGCGCG-TGCAGGAGGGCGGGGGCTCTGGTTGTAAGGCA 1139
Db      1178 GCAGGAGCCCAGCCAGCTGCGCCTGCGCTGCAGGAGGGCGGGGGCTCTGGTTGTAAAACA 1237

Qy      1140 CACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGACAGATGAC 1199
Db      1238 CACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGACAGATGAC 1297

Qy      1200 C 1200
Db      1298 C 1298
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RESULT 10
CS119692
LOCUS       CS119692                1323 bp    DNA     linear   PAT 08-JUL-2005
DEFINITION  Sequence 1739 from Patent WO2005054508.
ACCESSION   CS119692
VERSION     CS119692.1  GI:70667638
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Bertucci,F., Houlgatte,R., Birnbaum,D. and Debono,S.
  TITLE     Gene expression profiling of colon cancer by dna microarrays and
            correlation with survival and histoclinical parameters
  JOURNAL   Patent: WO 2005054508-A 1739 16-JUN-2005;
            Ipsogen (FR); Institut Paoli-Calmettes, Ipc (FR); Institut National
            de la Sante et de la Recherche Medicale (INSERM) (FR)
FEATURES             Location/Qualifiers
     source          1. .1323
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             98.4%;  Score 1181;  DB 6;  Length 1323;
  Best Local Similarity   99.5%;  Pred. No. 3.8e-271;
  Matches 1195;  Conservative    0;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          1 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60
Db         98 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 157

Qy         61 CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTG 120
Db        158 CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTG 217

Qy        121 GTGGCTGTGCGTTCTGGGGACCCTGGTGGGGCTCTCAGCTACTCCAGCCCCCAAGAGCTG 180
Db        218 GTGGCTGTGCGTTCTGGGGACCCTGGTGGGGCTCTCAGCTACTCCAGCCCCCAAGAGCTG 277

Qy        181 CCCAGAGAGGCACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240
Db        278 CCCAGAGAGGCACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 337

Qy        241 ATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 300
Db        338 ATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 397

Qy        301 GGGGGTCTCCTTCTCTCCTGACCACCACACCCGGCCCCACTGTGAGAGCTGTCGGCACTG 360
Db        398 GGGGGTCTCCTTCTCTCCTGACCACCACACCCGGCCCCACTGTGAGAGCTGTCGGCACTG 457

Qy        361 TAACTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCCTGTCG 420
Db        458 TAACTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCCTGTCG 517

Qy        421 CAATGGCTGGCAGTGCAGGGACAAGGAGTGCACCGAGTGTGATCCTCTTCCAAACCCTTC 480
Db        518 CAATGGCTGGCAGTGCAGGGACAAGGAGTGCACCGAGTGTGATCCTCTTCCAAACCCTTC 577

Qy        481 GCTGACCGCTCGGTCGTCTCAGGCCCTGAGCCCACACCCTCAGCCCACCCACTTACCTTA 540
Db        578 GCTGACCGCTCGGTCGTCTCAGGCCCTGAGCCCACACCCTCAGCCCACCCACTTACCTTA 637

Qy        541 TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAG 600
Db        638 TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAG 697

Qy        601 GCAGCTGCCTGCCCGGACTCTCTCTACCCACTGGCCACCCCAAAGATCCCTGTGCAGCTC 660
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Db        698 GCAGCTGCCTGCCCGGACTCTCTCTACCCACTGGCCACCCCAAAGATCCCTGTGCAGCTC 757

Qy        661 CGATTTTATTCGCATCCTTGTGATCTTCTCTGGAATGTTCCTTGTTTTCACCCTGGCCGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        758 CGATTTTATTCGCATCCTTGTGATCTTCTCTGGAATGTTCCTTGTTTTCACCCTGGCCGG 817

Qy        721 GGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAACAAAGGAGAAAGTCCTGTGGA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        818 GGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAACAAAGGAGAAAGTCCTGTGGA 877

Qy        781 GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAGCACCATCCCCAT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        878 GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAGCACCATCCCCAT 937

Qy        841 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGTAG 900
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        938 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGGAG 997

Qy        901 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        998 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 1057

Qy        961 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1058 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1117

Qy       1021 GAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGTGGAGAGTGGGAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1118 GAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGTGGAGAGTGGGAA 1177

Qy       1081 GCAGGAGCCCAGCCAGCTGCGCGCGCG-TGCAGGAGGGCGGGGGGCTCTGGTTGTAAGGCA 1139
              |||||||||||||||||||||  ||| |||||||||||||||||||||||||  ||
Db       1178 GCAGGAGCCCAGCCAGCTGCGCCTGCGCTGCAGGAGGGCGGGGGGCTCTGGTTGTAAAACA 1237

Qy       1140 CACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGACAGATGAC 1199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1238 CACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGACAGATGAC 1297

Qy       1200 C 1200
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Db       1298 C 1298
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RESULT 11
AY890880
LOCUS       AY890880               783 bp    mRNA    linear   SYN 21-MAR-2005
DEFINITION  Synthetic construct Homo sapiens clone FLH021597.01L tumor necrosis
            factor receptor superfamily member 7 (TNFRSF7) mRNA, partial cds.
ACCESSION   AY890880
VERSION     AY890880.1  GI:61366130
KEYWORDS    Human ORF Project.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 783)
  AUTHORS   Hines,L., Rolfs,A., Jepson,D., Moreira,D., Raphael,J., Kelley,F.,
            Shen,B., Halleck,A., Koundinya,M., Hu,Y., Zuo,D., Taycher,E.,
            Williamson,J. and LaBaer,J.
  TITLE     Cloning of human full-length CDS in Creator (TM) recombinational
            vector system
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 783)
  AUTHORS   Hines,L., Rolfs,A., Jepson,D., Moreira,D., Raphael,J., Kelley,F.,
            Shen,B., Halleck,A., Koundinya,M., Hu,Y., Zuo,D., Taycher,E.,
            Williamson,J. and LaBaer,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-JAN-2005) Biological Chemistry and Molecular
            Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
            Cambridge, MA 02141, USA
COMMENT     This CDS clone is a part of a collection of human full-length
            expression clones generated by Harvard Institute of Proteomics.
            This ORF clone has been cloned without stop-codon (to allow fusion
            with C-terminal tag). The CDS has been directionally cloned using
            BD In-Fusion(TM) cloning system between the SalI and HindIII sites
            of the pDNR-Dual vector. Additional sequences in the clone:  'ACC'
            after SalI site and before 'ATG' to provide Kozak consensus
            sequence; 'GG' after last codon and before HindIII site to maintain
            reading frame.  Each clone is clonally isolated and full-length
            sequence-verified.
FEATURES             Location/Qualifiers
     source          1. .783
                     /organism="synthetic construct"
                     /mol_type="mRNA"
                     /db_xref="taxon:32630"
                     /clone="FLH021597.01L"
                     /lab_host="Escherichia coli DH5alpha T1 resistant"
                     /note="derived from Homo sapiens first strand cDNA library
                     from placenta and brain"
     gene            1. .>783
                     /gene="TNFRSF7"
     CDS             1. .>783
                     /gene="TNFRSF7"
                     /codon_start=1
                     /transl_table=11
                     /product="tumor necrosis factor receptor superfamily
                     member 7"
                     /protein_id="AAX42818.1"
                     /db_xref="GI:61366131"
                     /translation="MARPHPWWLCVLGTLVGLSATPAPKSCPERHYWAQGKLCCQMCE
                     PGTFLVKDCDQHRKAAQCDPCIPGVSFSPDHHTRPHCESCRHCNSGLLVRNCTITANA
                     ECACRNGWQCRDKECTECDPLPNPSLTARSSQALSPHPQPTHLPYVSEMLEARTAGHM
                     QTLADFRQLPARTLSTHWPPQRSLCSSDFIRILVIFSGMFLVFTLAGALFLHQRRKYR
                     SNKGESPVEPAEPCRYSCPREEEGSTIPIQEDYQKPEPACSPL"
ORIGIN
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  Query Match             65.0%;  Score 779.4;  DB 11;  Length 783;
  Best Local Similarity   99.9%;  Pred. No. 3.2e-175;
  Matches  780;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         101 ATGGCACGGCCACATCCCTGGTGGCTGTGCGTTCTGGGGACCCTGGTGGGGCTCTCAGCT 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATGGCACGGCCACATCCCTGGTGGCTGTGCGTTCTGGGGACCCTGGTGGGGCTCTCAGCT 60

Qy         161 ACTCCAGCCCCCAAGAGCTGCCCAGAGAGGCACTACTGGGCTCAGGGAAAGCTGTGCTGC 220
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 ACTCCAGCCCCCAAGAGCTGCCCAGAGAGGCACTACTGGGCTCAGGGAAAGCTGTGCTGC 120

Qy         221 CAGATGTGTGAGCCAGGAACATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCT 280
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 CAGATGTGTGAGCCAGGAACATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCT 180

Qy         281 CAGTGTGATCCTTGCATACCGGGGGGTCTCCTTCTCTCCTGACCACCACACCCGGCCCCAC 340
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 CAGTGTGATCCTTGCATACCGGGGGTCTCCTTCTCTCCTGACCACCACACCCGGCCCCAC 240

Qy         341 TGTGAGAGCTGTCGGCACTGTAACTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCC 400
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 TGTGAGAGCTGTCGGCACTGTAACTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCC 300

Qy         401 AATGCTGAGTGTGCCTGTCGCAATGGCTGGCAGTGCAGGGACAAGGAGTGCACCGAGTGT 460
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 AATGCTGAGTGTGCCTGTCGCAATGGCTGGCAGTGCAGGGACAAGGAGTGCACCGAGTGT 360

Qy         461 GATCCTCTTCCAAACCCTTCGCTGACCGCTCGGTCGTCTCAGGCCCTGAGCCCACACCCT 520
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 GATCCTCTTCCAAACCCTTCGCTGACCGCTCGGTCGTCTCAGGCCCTGAGCCCACACCCT 420

Qy         521 CAGCCCACCCACTTACCTTATGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATG 580
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 CAGCCCACCCACTTACCTTATGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATG 480

Qy         581 CAGACTCTGGCTGACTTCAGGCAGCTGCCTGCCCGGACTCTCTCTACCCACTGGCCACCC 640
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 CAGACTCTGGCTGACTTCAGGCAGCTGCCTGCCCGGACTCTCTCTACCCACTGGCCACCC 540

Qy         641 CAAAGATCCCTGTGCAGCTCCGATTTTATTCGCATCCTTGTGATCTTCTCTGGAATGTTC 700
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CAAAGATCCCTGTGCAGCTCCGATTTATTCGCATCCTTGTGATCTTCTCTGGAATGTTC 600

Qy        701 CTTGTTTTCACCCTGGCCGGGGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAAC 760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTGTTTTCACCCTGGCCGGGGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAAC 660

Qy        761 AAAGGAGAAAGTCCTGTGGAGCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAG 820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAAGGAGAAAGTCCTGTGGAGCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAG 720

Qy        821 GAGGGCAGCACCATCCCCATCCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCC 880
              |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db        721 GAGGGCAGCACCATCCCCATCCAGGAGGATTACCAAAAACCGGAGCCTGCCTGCTCCCCC 780

Qy        881 T 881
              |
Db        781 T 781


RESULT 12
AX778265
LOCUS       AX778265                 524 bp    DNA     linear   PAT 14-JUL-2003
DEFINITION  Sequence 422 from Patent WO03039443.
ACCESSION   AX778265
VERSION     AX778265.1  GI:32695259
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Haferlach,T., Schoch,C., Kern,W., Kohlmann,A., Schnittger,S.,
            Dugas,M., Eils,R., Brors,B. and Mergenthaler,S.
  TITLE     Novel genetic markers for leukemias
  JOURNAL   Patent: WO 03039443-A 422 15-MAY-2003;
            Deutsches Krebsforschungszentrum (DE) ;
            Ludwig-Maximilian-Universitaet Muenchen (DE) ; Haferlach, Torsten,
            PD Dr. Dr. (DE) ; Schoch, Claudia (DE) ; Kern, Wolfgang (DE)
FEATURES             Location/Qualifiers
     source          1. .524
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             42.1%;  Score 505.6;  DB 6;  Length 524;
  Best Local Similarity   99.0%;  Pred. No. 8.1e-110;
  Matches  519;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy        649 CCTGTGCAGCTCCGATTTATTCGCATCCTTGTGATCTTCTCTGGAATGTTCCTTGTTTT 708
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCTGTGCAGCTCCGATTTATTCGCATCCTTGTGATCTTCTCTGGAATGTTCCTTGTTTT 60

Qy        709 CACCCTGGCCGGGGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAACAAAGGAGA 768
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCCTGGCCGGGGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAACAAAGGAGA 120

Qy        769 AAGTCCTGTGGAGCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAG 828
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGTCCTGTGGAGCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAG 180

Qy        829 CACCATCCCCATCCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAG 888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CACCATCCCCATCCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAG 240

Qy        889 CACCTGCGGTAGCTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGG 948
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CACCTGCGGTAGCTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGG 300

Qy        949 GAGAGTGAGACCTGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGT 1008
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAGAGTGAGACCTGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGT 360

Qy       1009 GTACACGTGACAGAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGT 1068
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTACACGTGACAGAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGT 420

Qy       1069 GGAGAGTGGGAAGCAGGAGCCCAGCCAGCTGCGCGCGCG-TGCAGGAGGGCGGGGCTCT 1127
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Db        421 GGAGAGTGGGAAGCAGGAGCCCAGCCAGCTGCGCCTGCGCTGCAGGAGGGCGGGGCTCT 480

Qy       1128 GGTTGTAAGGCACACTTCCTGCTGCGAAAGACCCACATGCTACA 1171
              ||||||||  ||||||||||||||||||||||||||||||||||
Db        481 GGTTGTAAAACACACTTCCTGCTGCGAAAGACCCACATGCTACA 524


RESULT 13
MUSCD27A
LOCUS       MUSCD27A                1585 bp    mRNA    linear   ROD 25-SEP-1993
DEFINITION  Mus musculus CD27 antigen (Cd27) mRNA.
ACCESSION   L24495
VERSION     L24495.1  GI:403146
KEYWORDS    CD27 antigen.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1585)
  AUTHORS   Gravestein,L.A., Blom,B., Nolten,L.A., de Vries,E., van der
            Horst,G., Ossendorp,F., Borst,J. and Loenen,W.A.
  TITLE     Cloning and expression of murine CD27: comparison with 4-1BB,
            another lymphocyte-specific member of the nerve growth factor
            receptor family
  JOURNAL   Eur. J. Immunol. 23 (4), 943-950 (1993)
   PUBMED   8384562
COMMENT     Original source text: Mus musculus (strain B6/CBAFIJ) (library:
            oligo dT in lambda ZAP) female Juvenile, 6-8 weeks thymus cDNA to
            mRNA.
FEATURES             Location/Qualifiers
     source          1. .1585
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="B6/CBAFIJ"
                     /db_xref="taxon:10090"
                     /sex="female"
                     /tissue_type="thymus"
                     /dev_stage="Juvenile, 6-8 weeks"
                     /tissue_lib="oligo dT in lambda ZAP"
ORIGIN

  Query Match             37.6%;  Score 451.8;  DB 9;  Length 1585;
  Best Local Similarity   73.2%;  Pred. No. 5e-97;
  Matches  633;  Conservative    0;  Mismatches  202;  Indels   30;  Gaps    3;

Qy         69 GGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTGGTGGCTGT 128
              |||| |||||| || |  ||||||||||  | |||||| |||||| |||||  ||||| |
Db        146 GGGCTCAGAAAAGATCTCCCTGGGCAGGAGCTATGGCATGGCCACCTCCCTACTGGCTCT 205

Qy        129 GCGTTCTGGGGACCCTGGTGGGGCTCTCAGCTACTCCAGCCCCCAAGAGCTGCCCAGAGA 188
              || | ||||||||| |||| || ||||||||||| | |||||| || ||||| ||||| |
Db        206 GCATGCTGGGGACCTTGGTAGGACTCTCAGCTACCCTAGCCCCAAACAGCTGTCCAGACA 265

Qy        189 GGCACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAACATTCCTCG 248
                ||||||||| ||  ||||   || ||||||| ||||||||||||||| |||||| | |
Db        266 AACACTACTGGACTGGGGGAGGACTCTGCTGCCGGATGTGTGAGCCAGGTACATTCTTTG 325

Qy        249 TGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACCGGGGGTCT 308
              ||||||||||||| ||  | ||||  ||||||||||||||||| || ||||| ||   ||
Db        326 TGAAGGACTGTGAACAAGACAGAACAGCTGCTCAGTGTGATCCCTGTATACCAGGCACCT 385

Qy        309 CCTTCTCTCCTGACCACCACACCCGGCCCCACTGTGAGAGCTGTCGGCACTGTAACTCTG 368
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Qy        369 GTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCCTGTCGCAATGGCT 428
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Qy        489 CTCGGTCGTCTCAGGCCCTGAGCCCACACCCTCAGCCCACCCACTTACCTTATGTCAGTG 548
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Qy        549 AGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAGGCAGCTGC 608
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Db        626 AGAAGC------------CATCCTGGCCCCTACA---------------CAGGCAGCTTC 658

Qy        609 CTGCCCGGACTCTCTCTACCCACTGGCCACCCCAAAGATCCCTGTGCAGCTCCGATTTTA 668
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Qy        669 TTCGCATCCTTGTGATCTTCTCTGGAATGTTCCTTGTTTTCACCCTGGCCGGGGCCCTGT 728
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Qy        729 TCCTCCATCAACGAAGGAAATATAGATCAAACAAAGGAGAAAGTCCTGTGGAGCCTGCAG 788
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Db        956 ACGAGGGGCCATCCACAGAGACCTC 980
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RESULT 14
BC095844
LOCUS       BC095844               1602 bp    mRNA    linear   ROD 25-JUL-2005
DEFINITION  Rattus norvegicus similar to CD27 antigen precursor - mouse, mRNA
            (cDNA clone MGC:112688 IMAGE:7389613), complete cds.
ACCESSION   BC095844
VERSION     BC095844.1  GI:63101136
KEYWORDS    MGC.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 1602)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
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            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1602)
  AUTHORS   .
  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (06-MAY-2005) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Drs. Josef Lazar  & Howard Jacob, Medical
            College of Wisconsin
            cDNA Library Preparation: Open Biosystems
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 227 Row: c Column: 6
            This clone was selected for full length sequencing because it
            passed the following selection criteria: Hexamer frequency ORF
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                     /lab_host="DH10B"
                     /note="Vector: pExpress1"
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ORIGIN
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  Query Match           36.3%;  Score 435.2;  DB 9;  Length 1602;
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  Matches  611;  Conservative    0;  Mismatches  188;  Indels   33;  Gaps    3;

Qy         69 GGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTGGTGGCTGT 128
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Db         32 GGGCTCAGAGAAGCTCTCCCTGAGCAGGAGCCATGGCATGGCCACCCCTCTACTGGCTCT 91

Qy        129 GCGTTCTGGGGGACCCTGGTGGGGCTCTCAGCTACTCCAGCCCCCAAGAGCTGCCCAGAGA 188
              || | ||||||||| |||| ||||||| ||||||  |||||||| || | ||| ||||| |
Db         92 GCATGCTGGGGACCTTGGTAGGGCTCTTAGCTACCCCAGCCCCAAACAACTGTCCAGACA 151

Qy        189 GGCACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAACATTCCTCG 248
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Db        152 GACACTACTGGATTGGGGCAGGACTCTGCTGCCAGATGTGTGGGCCAGGGACATTCCTTG 211

Qy        249 TGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACCGGGGGTCT 308

Db        212 TGAAGCACTGTGACCAGGACAGAGCCGCTGCTCAGTGTGATCCGTGTATTCCAGGCACGT 271

Qy        309 CCTTCTCTCCTGACCACCACACCCGGCCCCACTGTGAGAGCTGTCGGCACTGTAACTCTG 368

Db        272 CCTTCTCTCCAGACTACCACACCCGGCCCCACTGCGAGAGCTGCAGGCACTGTAACTCTG 331

Qy        369 GTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCCTGTCGCAATGGCT 428

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Qy        429 GGCAGTGCAGGGACAAGGAGTGCACCGAGTGTGATCCTCTTCCAAACCCTTCGCTGACCG 488

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Qy        726 TGTTCCTCCATCAACGAAGGAAATATAGATCAAACAAAGGAGAAAGTCCTGTGGAGCCTG 785

Db        665 TGTTCTTCCATCAAAGAAGAAATCATGGGCCA---AATGAAGATAGCCAGGCAGTACCTG 721

Qy        786 CAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAGCACCATCCCCATCCAGG 845

Db        722 AAGAGCTTTGTCCTTACAGCTGCCCTAGGGAGGAGGAGGGCAGTGTCATCCCTATCCAGG 781

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RESULT 15
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LOCUS AC006064 172571 bp DNA linear PRI 01-FEB-2003
DEFINITION Homo sapiens 12 PAC RP5-940J5 (Roswell Park Cancer Institute Human PAC Library) complete sequence.
ACCESSION AC006064
VERSION AC006064.10 GI:28191361
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 172571)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chiu,D., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Emerling,S., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Han,J., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Ioshikhes,I., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lee,E., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Marondel,I., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Merscher,S., Metzker,M., Miller,A., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Montgomery,K.T., Morgan,M., Morris,S., Moser,M., Neal,D., Nelson,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shim,C., Shooshtari,N., Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Kucherlapati,R., Weinstock,G. and Gibbs,R.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 172571)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (26-NOV-1998) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE 3 (bases 1 to 172571)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (07-APR-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE 4 (bases 1 to 172571)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (15-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE 5 (bases 1 to 172571)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (01-FEB-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT On Feb 1, 2003 this sequence version replaced gi:4572650.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.
Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST

(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL:
http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.

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repeat_region	3893. .3916
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repeat_region	3927. .4232
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STS	8519. .8823
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Search completed: December 7, 2005, 06:01:41
Job time : 6324 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 7, 2005, 00:47:12 ; Search time 810 Seconds
(without alignments)
9873.619 Million cell updates/sec

Title: US-09-836-544C-28
Perfect score: 1200
Sequence: 1 ggggtgcaaagaagagacag.....aaataaagtgacagatgacc 1200

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1200	100.0	1200	2	AAV63459	Aav63459 Human CD2
2	1200	100.0	1200	2	AAV81216	Aav81216 Human CD2
3	1200	100.0	1200	4	AAS03189	Aas03189 Human T-l
4	1200	100.0	1200	12	ADO49368	Ado49368 Human CD2
5	1200	100.0	1203	2	AAQ21183	Aaq21183 Encodes T
6	1196.8	99.7	1200	2	AAT14722	Aat14722 Human CD2
7	1196.8	99.7	1200	3	AAA50595	Aaa50595 Human cel
8	1182.6	98.5	1204	8	ABQ80112	Abq80112 Modumet c
9	1182.6	98.5	1204	8	ACA64893	Aca64893 Human CD2
10	1182.6	98.5	1204	10	ADD25535	Add25535 Binding d
11	1182.6	98.5	1204	10	ADL15014	Adl15014 Human T-c
12	1182.6	98.5	1204	11	ADI31701	Adi31701 Human cDN
13	1182.6	98.5	1204	12	ADQ19552	Adq19552 Human sof
14	1182.6	98.5	1204	13	ADS83768	Ads83768 Human lym
15	1182.6	98.5	1711	12	ADQ23741	Adq23741 Human sof
16	1181	98.4	1300	13	ABD32559	Abd32559 Human can
17	1181	98.4	1323	12	ADP10460	Adp10460 Reference
18	1179.4	98.3	1204	13	ADQ85319	Adq85319 Human tum
19	1179.4	98.3	1204	13	ACF87472	Acf87472 Human SIR
20	1057.4	88.1	1479	13	ACN42265	Acn42265 Human dia
21	783	65.2	783	14	ADV43499	Adv43499 Human psy
22	731.4	60.9	1148	13	ACN42266	Acn42266 Human dia
c 23	564.8	47.1	622	14	ACL60681	Acl60681 Human col
c 24	518.6	43.2	892	4	AAI85846	Aai85846 Human pol
25	505.6	42.1	524	10	ADF79866	Adf79866 Leukaemia
26	426	35.5	172570	6	ABQ88207	Abq88207 Human ost
27	424.4	35.4	26815	13	ABD32558	Abd32558 Human can
28	369.4	30.8	1290	13	ABD32557	Abd32557 Mouse can
29	361.2	30.1	516	13	ADU12719	Adu12719 Solid tum
c 30	235.8	19.7	483	4	AAI15981	Aai15981 Probe #59
c 31	235.8	19.7	483	4	ABA58384	Aba58384 Human foe
c 32	235.8	19.7	483	4	AAI38019	Aai38019 Probe #67
c 33	235.8	19.7	483	4	ABA27495	Aba27495 Probe #59
c 34	235.8	19.7	483	4	AAK32170	Aak32170 Human bon
c 35	235.8	19.7	483	4	AAK06489	Aak06489 Human bra
c 36	235.8	19.7	483	4	ABS31867	Abs31867 Human liv
c 37	235.8	19.7	483	6	ABS06937	Abs06937 Human gen
c 38	234.4	19.5	455	4	AAI25198	Aai25198 Probe #15
c 39	234.4	19.5	455	4	ABA70980	Aba70980 Human foe
c 40	234.4	19.5	455	4	AAI51177	Aai51177 Probe #19
c 41	234.4	19.5	455	4	ABA37400	Aba37400 Probe #15
c 42	234.4	19.5	455	4	AAK45226	Aak45226 Human bon
c 43	234.4	19.5	455	4	AAK19256	Aak19256 Human bra
c 44	234.4	19.5	455	4	ABS44899	Abs44899 Human liv
c 45	234.4	19.5	455	6	ABS19476	Abs19476 Human gen

ALIGNMENTS

RESULT 1
AAV63459
ID AAV63459 standard; cDNA; 1200 BP.
XX
AC AAV63459;
XX
DT 25-MAR-2003 (revised)
DT 07-JUN-1999 (first entry)
XX
DE Human CD27 antigen cDNA.
XX
KW CD27; cell surface antigen; human; T lymphocyte; cloning; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 101. .883
FT /*tag= a
FT sig_peptide 101. .160
FT /*tag= b
FT mat_peptide 161. .880
FT /*tag= c
XX
PN US5830731-A.
XX
PD 03-NOV-1998.
XX
PF 21-MAY-1997; 97US-00861205.
XX
PR 25-FEB-1988; 88US-00160416.
PR 13-JUL-1989; 89US-00379076.
PR 23-MAR-1990; 90US-00498809.
PR 13-JUL-1990; 90US-00553759.
PR 01-DEC-1992; 92US-00983647.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Seed B, Aruffo A;
XX
DR WPI; 1998-609251/51.
DR P-PSDB; AAW80451.
XX

```
PT   New cloning vector and poly:linker - based on existing sequences for
PT   efficient cloning and expression of mammalian cDNA(s), especially human
PT   lymphocyte antigenic sequences.
XX
PS   Example 13; Col 65-66; 75pp; English.
XX
CC   This nucleotide sequence comprises human CD27 cDNA. The cDNA was isolated
CC   from a human T lymphocyte cDNA library using a novel method for cloning
CC   cDNAs from mammalian expression libraries. The method is based on
CC   transient expression of an antigen in eukaryotic cells and physical
CC   selection of cells expressing the antigen by adhesion to an antibody-
CC   coated substrate. The method is useful for the isolation and molecular
CC   cloning of any protein which can be expressed and transported to the cell
CC   surface membrane of a eukaryotic cell. It has been used to clone genes
CC   (see AAV63442-63) encoding cell surface antigens from mammalian
CC   lymphocytes (see AAW80440-55). The purified genes and proteins are useful
CC   for immunodiagnostic and immunotherapeutic applications, including the
CC   diagnosis and treatment of immune-mediated infections, diseases, and
CC   disorders of animals, including humans. CD27 (see AAW80451), a T
CC   lymphocyte activation antigen, has been expressed in COS cells. (Updated
CC   on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 1200 BP; 260 A; 373 C; 341 G; 226 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 1200;  DB 2;  Length 1200;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1200;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60

Qy         61 CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTG 120

Qy        121 GTGGCTGTGCGTTCTGGGGACCCTGGTGGGGCTCTCAGCTACTCCAGCCCCCAAGAGCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGGCTGTGCGTTCTGGGGACCCTGGTGGGGCTCTCAGCTACTCCAGCCCCCAAGAGCTG 180

Qy        181 CCCAGAGAGGCACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCCAGAGAGGCACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240

Qy        241 ATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 300

Qy        301 GGGGGTCTCCTTCTCTCCTGACCACCACACCCGGCCCCACTGTGAGAGCTGTCGGCACTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGGGGTCTCCTTCTCTCCTGACCACCACACCCGGCCCCACTGTGAGAGCTGTCGGCACTG 360

Qy        361 TAACTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCCTGTCG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TAACTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCCTGTCG 420

Qy        421 CAATGGCTGGCAGTGCAGGGACAAGGAGTGCACCGAGTGTGATCCTCTTCCAAACCCTTC 480
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Db        421 CAATGGCTGGCAGTGCAGGGACAAGGAGTGCACCGAGTGTGATCCTCTTCCAAACCCTTC 480

Qy        481 GCTGACCGCTCGGTCGTCTCAGGCCCTGAGCCCACACCCTCAGCCCACCCACTTACCTTA 540
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Db        481 GCTGACCGCTCGGTCGTCTCAGGCCCTGAGCCCACACCCTCAGCCCACCCACTTACCTTA 540

Qy        541 TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAG 600

Qy        601 GCAGCTGCCTGCCCGGACTCTCTCTACCCACTGGCCACCCCAAAGATCCCTGTGCAGCTC 660
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Db        601 GCAGCTGCCTGCCCGGACTCTCTCTACCCACTGGCCACCCCAAAGATCCCTGTGCAGCTC 660

Qy        661 CGATTTTATTCGCATCCTTGTGATCTTCTCTGGAATGTTCCTTGTTTTCACCCTGGCCGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGATTTTATTCGCATCCTTGTGATCTTCTCTGGAATGTTCCTTGTTTTCACCCTGGCCGG 720

Qy        721 GGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAACAAAGGAGAAAGTCCTGTGGA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAACAAAGGAGAAAGTCCTGTGGA 780

Qy        781 GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAGCACCATCCCCAT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAGCACCATCCCCAT 840

Qy        841 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGTAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGTAG 900

Qy        901 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 960

Qy        961 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020

Qy       1021 GAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGTGGAGAGTGGGAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGTGGAGAGTGGGAA 1080

Qy       1081 GCAGGAGCCCAGCCAGCTGCGCGCGCGTGCAGGAGGGCGGGGGCTCTGGTTGTAAGGCAC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GCAGGAGCCCAGCCAGCTGCGCGCGCGTGCAGGAGGGCGGGGGCTCTGGTTGTAAGGCAC 1140

Qy       1141 ACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGACAGATGACC 1200
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Db       1141 ACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGACAGATGACC 1200


RESULT 2
AAV81216
ID   AAV81216 standard; cDNA; 1200 BP.
XX
AC   AAV81216;
XX
DT   10-MAY-1999  (first entry)
XX
DE   Human CD27 antigen cDNA.
XX
KW   CD27; cell surface antigen; human; T lymphocyte; cDNA library; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             101. .883
FT                   /*tag=  a
FT   sig_peptide     101. .160
FT                   /*tag=  b
FT   mat_peptide     161. .880
FT                   /*tag=  c
XX
PN   US5849898-A.
XX
PD   15-DEC-1998.
XX
PF   07-JUN-1995;   95US-00485447.
XX
PR   25-FEB-1988;   88US-00160416.
PR   13-JUL-1989;   89US-00379076.
PR   23-MAR-1990;   90US-00498809.
PR   13-JUL-1990;   90US-00553759.
PR   01-DEC-1992;   92US-00983647.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Seed B,  Oquendo C,  Camerini D,  Stamenkovic I,  Stengelin S;
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PI   Amiot M,  Lauffer L,  Allen J,  Simmons D,  Aruffo A;
XX
DR   WPI; 1999-069813/06.
DR   P-PSDB; AAW86198.
XX
PT   cDNA encoding human CD40 antigen - useful for cloning cDNA encoding cell
PT   surface antigens, constructing cDNA libraries, expressing vectors for
PT   expression in eukaryotic cells or their fragments.
XX
PS   Example 13; Col 65-66; 79pp; English.
XX
CC   This nucleotide sequence comprises human CD27 cDNA. The cDNA was isolated
CC   from a human T lymphocyte cDNA library using a novel method for cloning
CC   cDNAs from mammalian expression libraries. The method is based on
CC   transient expression of an antigen in eukaryotic cells and physical
CC   selection of cells expressing the antigen by adhesion to an antibody-
CC   coated substrate. The method is useful for the isolation and molecular
CC   cloning of any protein which can be expressed and transported to the cell
CC   surface membrane of a eukaryotic cell. It has been used to clone genes
CC   (see AAV81198-220) encoding cell surface antigens such as CD1a, CD1b,
CC   CD1c, CD2, CD6, CD7, CD13, CD14, CD16, CD19, CD20, CD22, CD26, CD27,
CC   CD28, CD31, CDw32a, CDw32b, CD33, CD34, CD36, CD37, CD38, CD39, CD40,
CC   CD43, CD44, CD53, ICAM, LFA-3, FcRIa, FcRIb, TliSa and Leu8 (see AAW86188
CC   -62, AAW89151-52 and AAW88451). CD40 cDNA (see AAV81198) is specifically
CC   claimed. CD27, a T lymphocyte activation antigen, has been expressed in
CC   COS cells
XX
SQ   Sequence 1200 BP; 260 A; 373 C; 341 G; 226 T; 0 U; 0 Other;

  Query Match          100.0%;  Score 1200;  DB 2;  Length 1200;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1200;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60

Qy         61 CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTG 120
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Qy        121 GTGGCTGTGCGTTCTGGGGACCCTGGTGGGGCTCTCAGCTACTCCAGCCCCCAAGAGCTG 180
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Qy        181 CCCAGAGAGGCACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240
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Db        241 ATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 300

Qy        301 GGGGGTCTCCTTCTCTCCTGACCACCACACCCGGCCCCACTGTGAGAGCTGTCGGCACTG 360
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Qy        421 CAATGGCTGGCAGTGCAGGGACAAGGAGTGCACCGAGTGTGATCCTCTTCCAAACCCTTC 480
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Db        421 CAATGGCTGGCAGTGCAGGGACAAGGAGTGCACCGAGTGTGATCCTCTTCCAAACCCTTC 480

Qy        481 GCTGACCGCTCGGTCGTCTCAGGCCCTGAGCCCACACCCTCAGCCCACCCACTTACCTTA 540
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Qy        541 TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAG 600
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Db        541 TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAG 600

Qy        601 GCAGCTGCCTGCCCGGACTCTCTCTACCCACTGGCCACCCCAAAGATCCCTGTGCAGCTC 660
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Db        601 GCAGCTGCCTGCCCGGACTCTCTCTACCCACTGGCCACCCCAAAGATCCCTGTGCAGCTC 660

Qy        661 CGATTTTATTCGCATCCTTGTGATCTTCTCTGGAATGTTCCTTGTTTTCACCCTGGCCGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGATTTTATTCGCATCCTTGTGATCTTCTCTGGAATGTTCCTTGTTTTCACCCTGGCCGG 720

Qy        721 GGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAACAAAGGAGAAAGTCCTGTGGA 780
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Db        721 GGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAACAAAGGAGAAAGTCCTGTGGA 780

Qy        781 GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAGCACCATCCCCAT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAGCACCATCCCCAT 840

Qy        841 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGTAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGTAG 900

Qy        901 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 960

Qy        961 TGGCAGCCACAACTGCAGTCCCATCCTCCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020
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Db        961 TGGCAGCCACAACTGCAGTCCCATCCTCCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020

Qy       1021 GAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGTGGAGAGTGGGAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGTGGAGAGTGGGAA 1080

Qy       1081 GCAGGAGCCCAGCCAGCTGCGCGCGCGTGCAGGAGGGCGGGGGCTCTGGTTGTAAGGCAC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GCAGGAGCCCAGCCAGCTGCGCGCGCGTGCAGGAGGGCGGGGGCTCTGGTTGTAAGGCAC 1140

Qy       1141 ACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGACAGATGACC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGACAGATGACC 1200

RESULT 3
AAS03189
ID   AAS03189 standard; cDNA; 1200 BP.
XX
AC   AAS03189;
XX
DT   29-AUG-2001  (first entry)
XX
DE   Human T-lymphocyte specific antigen CD27 cDNA sequence.
XX
KW   Human; T-lymphocyte specific antigen; immune-mediated disease; CD27;
KW   infection; immune deficiency disorder; hypersensitivity; inflammation;
KW   systemic lupus erythematosus; platelet disorder; rheumatoid arthritis;
KW   transplant rejection; asthma; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             101. .883
FT                   /*tag=  a
FT                   /product= "CD27 antigen"
FT                   /transl_except= (pos:200. .202,aa:Arg)
FT   sig_peptide     101. .160
FT                   /*tag=  b
FT   mat_peptide     161. .880
FT                   /*tag=  c
XX
PN   US6218525-B1.
XX
PD   17-APR-2001.
XX
PF   01-DEC-1992;   92US-00983647.
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XX
PR   25-FEB-1988;   88US-00160416.
PR   13-JUL-1989;   89US-00379076.
PR   13-JUL-1990;   90US-00553759.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Seed B,  Aruffo A,  Simmons D;
XX
DR   WPI; 2001-289848/30.
DR   P-PSDB; AAU02446.
XX
PT   New recombinant DNA encoding CD28 useful for diagnosing and treating
PT   immune-mediated diseases, infections or disorders, e.g. systemic lupus
PT   erythematosus, asthma, transplant rejection, rheumatoid arthritis.
XX
PS   Example 13; Col 61-62; 72pp; English.
XX
CC   The present sequence encoding for human T-lymphocyte specific antigen
CC   CD27 is 1 of various human lymphocyte cell surface antigen cDNA sequences
CC   (AAS03172, AAS03173, AAS03175-AAS03195) described in the present
CC   invention. The invention relates to a novel method of cloning cDNA
CC   encoding cell surface antigens and efficient construction of cDNA
CC   libraries. Also described are 2 expression vectors (AAS03171, AAS03174)
CC   which provide high level expression in eukaryotic host cells. A
CC   genetically engineered cDNA sequence encoding the CD28 amino acid
CC   extracellular domain sequence (amino acids 1-134 given in AAU02437)
CC   and/or comprising nucleotides 100-759, 154-555 or 154-759 of the CD28
CC   cDNA sequence (AAS03175) is also new. The purified genes and proteins are
CC   useful for immunodiagnostic and immunotherapeutic applications, such as
CC   in the diagnosis and treatment of immune-mediated diseases, infections or
CC   disorders in animals and humans. Such diseases include immune deficiency
CC   diseases, diseases of immediate type of hypersensitivity, asthma,
CC   hypersensitivity pneumonitis, systemic lupus erythematosus, rheumatoid
CC   arthritis, acute and chronic inflammation, platelet disorders, plasma and
CC   other cell neoplasms, parasitic diseases, multiple sclerosis, Guillain-
CC   Barre syndrome and tissue and organ transplant rejection. The sequences
CC   can also be used to identify, isolate and purify other antibodies and
CC   antigens
XX
SQ   Sequence 1200 BP; 260 A; 373 C; 341 G; 226 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 1200;  DB 4;  Length 1200;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1200;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60

Qy         61 CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTG 120

Qy        121 GTGGCTGTGCGTTCTGGGGACCCTGGTGGGGCTCTCAGCTACTCCAGCCCCCAAGAGCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGGCTGTGCGTTCTGGGGACCCTGGTGGGGCTCTCAGCTACTCCAGCCCCCAAGAGCTG 180

Qy        181 CCCAGAGAGGCACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCCAGAGAGGCACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240

Qy        241 ATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 300

Qy        301 GGGGGTCTCCTTCTCTCCTGACCACCACACCCGGCCCCACTGTGAGAGCTGTCGGCACTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGGGGTCTCCTTCTCTCCTGACCACCACACCCGGCCCCACTGTGAGAGCTGTCGGCACTG 360

Qy        361 TAACTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCCTGTCG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TAACTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCCTGTCG 420

Qy        421 CAATGGCTGGCAGTGCAGGGACAAGGAGTGCACCGAGTGTGATCCTCTTCCAAACCCTTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGCTGGCAGTGCAGGGACAAGGAGTGCACCGAGTGTGATCCTCTTCCAAACCCTTC 480

Qy        481 GCTGACCGCTCGGTCGTCTCAGGCCCTGAGCCCACACCCTCAGCCCACCCACTTACCTTA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCTGACCGCTCGGTCGTCTCAGGCCCTGAGCCCACACCCTCAGCCCACCCACTTACCTTA 540

Qy        541 TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAG 600

Qy        601 GCAGCTGCCTGCCCGGACTCTCTCTACCCACTGGCCACCCCAAAGATCCCTGTGCAGCTC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCAGCTGCCTGCCCGGACTCTCTCTACCCACTGGCCACCCCAAAGATCCCTGTGCAGCTC 660

Qy        661 CGATTTTATTCGCATCCTTGTGATCTTCTCTGGAATGTTCCTTGTTTTCACCCTGGCCGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGATTTTATTCGCATCCTTGTGATCTTCTCTGGAATGTTCCTTGTTTTCACCCTGGCCGG 720

Qy        721 GGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAACAAAGGAGAAAGTCCTGTGGA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAACAAAGGAGAAAGTCCTGTGGA 780

Qy        781 GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAGCACCATCCCCAT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAGCACCATCCCCAT 840

Qy        841 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGTAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGTAG 900

Qy        901 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 960

Qy        961 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020

Qy       1021 GAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGTGGAGAGTGGGAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGTGGAGAGTGGGAA 1080

Qy       1081 GCAGGAGCCCAGCCAGCTGCGCGCGCGTGCAGGAGGGCGGGGGCTCTGGTTGTAAGGCAC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GCAGGAGCCCAGCCAGCTGCGCGCGCGTGCAGGAGGGCGGGGGCTCTGGTTGTAAGGCAC 1140

Qy       1141 ACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGACAGATGACC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGACAGATGACC 1200


RESULT 4
ADO49368
ID   ADO49368 standard; cDNA; 1200 BP.
XX
AC   ADO49368;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Human CD27 cDNA.
XX
KW   cell surface antigen; immune-mediated disorder; asthma;
KW   rheumatoid arthritis; multiple sclerosis; vasculitis; inflammation; ss;
KW   gene; human.
XX
OS   Homo sapiens.
XX
PN   US2004072283-A1.
XX
PD   15-APR-2004.
```

XX
PF 17-APR-2001; 2001US-00836544.
XX
PR 25-FEB-1988; 88US-00160416.
PR 13-JUL-1989; 89US-00379076.
PR 23-MAR-1990; 90US-00498809.
PR 13-JUL-1990; 90US-00553759.
PR 01-DEC-1992; 92US-00983647.
XX
PA (SEED/) SEED B.
PA (ALLE/) ALLEN J.
PA (ARUF/) ARUFFO A.
PA (CAME/) CAMERINI D.
PA (LAUF/) LAUFFER L.
PA (OQUE/) OQUENDO C.
PA (SIMM/) SIMMONS D.
PA (STAM/) STAMENKOVIC I.
PA (STEN/) STENGELIN S.
PA (AMIO/) AMIOT M.
XX
PI Seed B, Allen J, Aruffo A, Camerini D, Lauffer L, Oquendo C;
PI Simmons D, Stamenkovic I, Stengelin S, Amiot M;
XX
DR WPI; 2004-328571/30.
DR P-PSDB; ADO49369.
XX
PT New cloning cDNA segments encoding cell surface antigens of human
PT lymphocytes, useful in diagnosing and treating asthma, rheumatoid
PT arthritis, multiple sclerosis, vasculitis and inflammation and
PT infections.
XX
PS Claim 1; Page 33-34; 75pp; English.
XX
CC The invention relates to a cloned cDNA segment encoding a cell surface
CC antigen selected from CD1a, CD1b, CD1c, CD2, CD6, CD7, CD13, CD14, CD16,
CC CD19, CD20, CD22, CD26, CD27, CD31, CD2w32a, CDw32b, CD33, CD34, CD36,
CC CD37, CD38, CD39, CD40, CD43 and their functional derivatives. The cell
CC surface antigens of human lymphocytes prepared from the cDNAs are useful
CC in diagnostic and therapeutic utility in immune-mediated disorders
CC (asthma, rheumatoid arthritis, multiple sclerosis, vasculitis and
CC inflammation) and infections in mammals, including humans. The present
CC sequence represents a human cell surface antigen cDNA.
XX
SQ Sequence 1200 BP; 260 A; 373 C; 341 G; 226 T; 0 U; 0 Other;

Query Match 100.0%; Score 1200; DB 12; Length 1200;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60

Qy         61 CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTG 120

Qy        121 GTGGCTGTGCGTTCTGGGGACCCTGGTGGGGCTCTCAGCTACTCCAGCCCCCAAGAGCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGGCTGTGCGTTCTGGGGACCCTGGTGGGGCTCTCAGCTACTCCAGCCCCCAAGAGCTG 180

Qy        181 CCCAGAGAGGCACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCCAGAGAGGCACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240

Qy        241 ATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 300

Qy        301 GGGGGTCTCCTTCTCTCCTGACCACCACACCCGGCCCCACTGTGAGAGCTGTCGGCACTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGGGGTCTCCTTCTCTCCTGACCACCACACCCGGCCCCACTGTGAGAGCTGTCGGCACTG 360

Qy        361 TAACTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCCTGTCG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TAACTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCCTGTCG 420

Qy        421 CAATGGCTGGCAGTGCAGGGACAAGGAGTGCACCGAGTGTGATCCTCTTCCAAACCCTTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGCTGGCAGTGCAGGGACAAGGAGTGCACCGAGTGTGATCCTCTTCCAAACCCTTC 480

Qy        481 GCTGACCGCTCGGTCGTCTCAGGCCCTGAGCCCACACCCTCAGCCCACCCACTTACCTTA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCTGACCGCTCGGTCGTCTCAGGCCCTGAGCCCACACCCTCAGCCCACCCACTTACCTTA 540

Qy        541 TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAG 600

Qy        601 GCAGCTGCCTGCCCGGACTCTCTCTACCCACTGGCCACCCCAAAGATCCCTGTGCAGCTC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCAGCTGCCTGCCCGGACTCTCTCTACCCACTGGCCACCCCAAAGATCCCTGTGCAGCTC 660

Qy        661 CGATTTTATTCGCATCCTTGTGATCTTCTCTGGAATGTTCCTTGTTTTCACCCTGGCCGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGATTTTATTCGCATCCTTGTGATCTTCTCTGGAATGTTCCTTGTTTTCACCCTGGCCGG 720

Qy        721 GGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAACAAAGGAGAAAGTCCTGTGGA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAACAAAGGAGAAAGTCCTGTGGA 780

Qy        781 GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAGCACCATCCCCAT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAGCACCATCCCCAT 840

Qy        841 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGTAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGTAG 900

Qy        901 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 960

Qy        961 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020

Qy       1021 GAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGTGGAGAGTGGGAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGTGGAGAGTGGGAA 1080

Qy       1081 GCAGGAGCCCAGCCAGCTGCGCGCGCGTGCAGGAGGGCGGGGGCTCTGGTTGTAAGGCAC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GCAGGAGCCCAGCCAGCTGCGCGCGCGTGCAGGAGGGCGGGGGCTCTGGTTGTAAGGCAC 1140

Qy       1141 ACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGACAGATGACC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGACAGATGACC 1200
```

RESULT 5
AAQ21183
ID AAQ21183 standard; DNA; 1203 BP.
XX
AC AAQ21183;
XX
DT 25-MAR-2003 (revised)
DT 21-MAY-1992 (first entry)
XX
DE Encodes T lymphocyte-specific CD27 Antigen.
XX
KW Rapid immunoselection cloning technique; cell surface antigen;
KW carcinoma antigen CD40; ss.
XX
OS Homo sapiens.
XX

```
FH   Key             Location/Qualifiers
FT   sig_peptide     101. .160
FT                   /*tag= a
FT   mat_peptide     161. .880
FT                   /*tag= b
XX
PN   WO9201049-A.
XX
PD   23-JAN-1992.
XX
PF   13-JUL-1990;   90US-00553759.
XX
PR   13-JUL-1990;   90US-00553759.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Seed B, Aruffo A, Amiot M;
XX
DR   WPI; 1992-056864/07.
DR   P-PSDB; AAR20814.
XX
PT   New CD53 cell surface antigen and DNA encoding it - for immuno-therapy
PT   and diagnosis of haematopoietic neoplasms, etc.
XX
PS   Example 13; Page 103; 160pp; English.
XX
CC   A cDNA clone encoding CD27 was obtained from human T lymphocyte cDNA
CC   transferred into COS cells and immunoselected using the MAbs OKT18a and
CC   CLB-9F4 (see e.g. AAQ21164 for description of the rapid immunoselection
CC   cloning method). A positive vector contained a 1.2kb insert. The ability
CC   to interfere with the binding of CD27 positive T cells with antigen
CC   presenting cells, or the ability to cause such binding to occur on
CC   surfaces other than lymphocyte cells, can be useful in diagnostics and
CC   therapy. (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ   Sequence 1203 BP; 261 A; 375 C; 341 G; 226 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 1200;  DB 2;  Length 1203;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1200;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60

Qy         61 CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTG 120

Qy        121 GTGGCTGTGCGTTCTGGGGACCCTGGTGGGGCTCTCAGCTACTCCAGCCCCCAAGAGCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGGCTGTGCGTTCTGGGGACCCTGGTGGGGCTCTCAGCTACTCCAGCCCCCAAGAGCTG 180

Qy        181 CCCAGAGAGGCACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCCAGAGAGGCACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240

Qy        241 ATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 300

Qy        301 GGGGGTCTCCTTCTCTCCTGACCACCACACCCGGCCCCACTGTGAGAGCTGTCGGCACTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGGGGTCTCCTTCTCTCCTGACCACCACACCCGGCCCCACTGTGAGAGCTGTCGGCACTG 360

Qy        361 TAACTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCCTGTCG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TAACTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCCTGTCG 420

Qy        421 CAATGGCTGGCAGTGCAGGGACAAGGAGTGCACCGAGTGTGATCCTCTTCCAAACCCTTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGCTGGCAGTGCAGGGACAAGGAGTGCACCGAGTGTGATCCTCTTCCAAACCCTTC 480

Qy        481 GCTGACCGCTCGGTCGTCTCAGGCCCTGAGCCCACACCCTCAGCCCACCCACTTACCTTA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCTGACCGCTCGGTCGTCTCAGGCCCTGAGCCCACACCCTCAGCCCACCCACTTACCTTA 540

Qy        541 TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAG 600

Qy        601 GCAGCTGCCTGCCCGGACTCTCTCTACCCACTGGCCACCCCAAAGATCCCTGTGCAGCTC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCAGCTGCCTGCCCGGACTCTCTCTACCCACTGGCCACCCCAAAGATCCCTGTGCAGCTC 660

Qy        661 CGATTTTATTCGCATCCTTGTGATCTTCTCTGGAATGTTCCTTGTTTTCACCCTGGCCGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGATTTTATTCGCATCCTTGTGATCTTCTCTGGAATGTTCCTTGTTTTCACCCTGGCCGG 720

Qy        721 GGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAACAAAGGAGAAAGTCCTGTGGA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAACAAAGGAGAAAGTCCTGTGGA 780

Qy        781 GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAGCACCATCCCCAT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAGCACCATCCCCAT 840

Qy        841 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGTAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGTAG 900

Qy        901 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 960

Qy        961 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020

Qy       1021 GAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGTGGAGAGTGGGAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGTGGAGAGTGGGAA 1080

Qy       1081 GCAGGAGCCCAGCCAGCTGCGCGCGCGTGCAGGAGGGCGGGGGCTCTGGTTGTAAGGCAC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GCAGGAGCCCAGCCAGCTGCGCGCGCGTGCAGGAGGGCGGGGGCTCTGGTTGTAAGGCAC 1140

Qy       1141 ACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGACAGATGACC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGACAGATGACC 1200


RESULT 6
AAT14722
ID   AAT14722 standard; cDNA; 1200 BP.
XX
AC   AAT14722;
XX
DT   25-MAR-2003  (revised)
DT   31-OCT-1996  (first entry)
XX
DE   Human CD27 antigen cDNA.
XX
KW   Cell surface antigen; cloning; immunoselection; immunotherapy; therapy;
KW   diagnosis; vector; COS; CD27; T-lymphocyte; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             101. .883
FT                   /*tag= a
FT                   /transl_except= (200. .202, aa:Arg)
FT                   /transl_except= (413. .415, aa: Ala)
FT   sig_peptide     101. .160
FT                   /*tag= b
FT   mat_peptide     161. .880
```

```
FT                   /*tag=  c
FT   misc_difference 742
FT                   /*tag=  d
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FT                   given in the specification, but interrupts the reading
FT                   frame"
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PN   US5506126-A.
XX
PD   09-APR-1996.
XX
PF   18-OCT-1993;   93US-00139273.
XX
PR   25-FEB-1988;   88US-00160416.
PR   13-JUL-1989;   89US-00379076.
PR   13-JUL-1990;   90US-00553759.
PR   01-DEC-1992;   92US-00983647.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Seed B,  Aruffo A;
XX
DR   WPI; 1996-200279/20.
DR   P-PSDB; AAR91441.
XX
PT   Cloning of cDNA encoding cell surface antigen - useful for isolation of
PT   diagnostic and therapeutic proteins.
XX
PS   Example 13; Col 67-68; 79pp; English.
XX
CC   A cDNA clone (AAT14722) codes for human antigen CD27 (AAR91441), a T-
CC   lymphocyte activation antigen. It was obtd. by constructing an expression
CC   library in COS cells using T-lymphocyte cDNA, and immunoselecting with
CC   monoclonal antibodies OKT18a and CLB-9F4. This immunoselection cloning
CC   method, developed to clone genes for cell surface antigens of human
CC   lymphocytes (see also AAT14703-04 and AAT14706-26), has general appln.
CC   Cell surface antigens are obtd. for diagnostic and therapeutic use.
CC   (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 1200 BP; 259 A; 372 C; 342 G; 227 T; 0 U; 0 Other;

  Query Match             99.7%;  Score 1196.8;  DB 2;  Length 1200;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1198;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60
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Db          1 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60

Qy         61 CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTG 120
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Db         61 CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTG 120

Qy        121 GTGGCTGTGCGTTCTGGGGACCCTGGTGGGGCTCTCAGCTACTCCAGCCCCCAAGAGCTG 180
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Db        121 GTGGCTGTGCGTTCTGGGGACCCTGGTGGGGCTCTCAGCTACTCCAGCCCCCAAGAGCTG 180

Qy        181 CCCAGAGAGGCACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240
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Db        181 CCCAGAGAGGCACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240

Qy        241 ATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 300
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Qy        301 GGGGGTCTCCTTCTCTCCTGACCACCACACCCGGCCCCACTGTGAGAGCTGTCGGCACTG 360
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Db        301 GGGGGTCTCCTTCTCTCCTGACCACCACACCCGGCCCCACTGTGAGAGCTGTCGGCACTG 360

Qy        361 TAACTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCCTGTCG 420
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Qy        421 CAATGGCTGGCAGTGCAGGGACAAGGAGTGCACCGAGTGTGATCCTCTTCCAAACCCTTC 480
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Qy        541 TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAG 600
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Qy        781 GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAGCACCATCCCCAT 840
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Db        841 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGTAG 900

Qy        901 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 960
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Db        901 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 960

Qy        961 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020
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Db        961 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020

Qy       1021 GAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGTGGAGAGTGGGAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGTGGAGAGTGGGAA 1080

Qy       1081 GCAGGAGCCCAGCCAGCTGCGCGCGCGTGCAGGAGGGCGGGGGCTCTGGTTGTAAGGCAC 1140
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Qy       1141 ACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGACAGATGACC 1200
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RESULT 7
AAA50595
ID   AAA50595 standard; cDNA; 1200 BP.
XX
AC   AAA50595;
XX
DT   19-DEC-2000  (first entry)
XX
DE   Human cell surface antigen CD27 cDNA.
XX
KW   CD27; cell surface antigen; human; immunoselection; panning;
KW   immunodiagnosis; diagnosis; immunotherapy; gene therapy; immune disorder;
KW   infection; asthma; immune-complex disease; amyloidosis;
KW   multiple sclerosis; parasitic disease; autoimmune disease; T-lymphocyte;
KW   ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             101. .883
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PD   29-AUG-2000.
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PF   28-OCT-1998;   98US-00181612.
XX
PR   25-FEB-1988;   88US-00160416.
PR   13-JUL-1989;   89US-00379076.
PR   23-MAR-1990;   90US-00498809.
PR   13-JUL-1990;   90US-00553759.
PR   01-DEC-1992;   92US-00983647.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Stamenkovic I,  Seed B;
XX
DR   WPI; 2000-586382/55.
DR   P-PSDB; AAY96137.
XX
PT   Isolated nucleic acid molecule encoding the CD19 cell surface antigen,
PT   useful for immunodiagnosis and immunotherapy of immune-mediated
PT   infections or disorders, e.g. asthma, immune-complex disease, parasitic
PT   diseases.
XX
PS   Example 13; Col 67-68; 75pp; English.
XX
CC   The present sequence is that of cDNA encoding human cell surface antigen
CC   (CSA) CD27 (see AAY96137), a T-lymphocyte activation antigen. The cDNA
CC   was isolated from a human T-lymphocyte cDNA introduced into COS cells and
CC   screened using a novel method of the invention. The method, designed to
CC   isolate CSA nucleic acids, is based upon transient expression of a CSA in
CC   eukaryotic cells and physical selection of cells expressing the antigen
CC   by adhesion to (panning on) an antibody-coated substrate such as a
CC   culture dish. CSA nucleic acids isolated by the method of the invention,
CC   and the proteins they encode, are useful for immunodiagnostic and
CC   immunotherapeutic applications, including the diagnosis and treatment of
CC   immune-mediated infections, diseases, and disorders in animals, including
CC   humans. These disorders include asthma, immune-complex disease,
CC   amyloidosis, parasitic diseases or multiple sclerosis. The ability to
CC   interfere with the binding of CD27 positive T cells with antigen
CC   presenting cells, or the ability to cause such binding to occur on
CC   surfaces other than lymphocyte cells, can be useful in diagnostics and
CC   therapy. A soluble CD27 fusion protein will be useful to prevent
CC   undesired T cell proliferation in certain autoimmune diseases
XX
SQ   Sequence 1200 BP; 260 A; 371 C; 343 G; 226 T; 0 U; 0 Other;

  Query Match             99.7%;  Score 1196.8;  DB 3;  Length 1200;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1198;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60
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Qy         61 CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTG 120
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Qy        121 GTGGCTGTGCGTTCTGGGGACCCTGGTGGGGCTCTCAGCTACTCCAGCCCCCAAGAGCTG 180
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Qy        181 CCCAGAGAGGCACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240
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Db        181 CCCAGAGAGGCACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240

Qy        241 ATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 300
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Db        241 ATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 300

Qy        301 GGGGGTCTCCTTCTCTCCTGACCACCACACCCGGCCCCACTGTGAGAGCTGTCGGCACTG 360
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Qy        481 GCTGACCGCTCGGTCGTCTCAGGCCCTGAGCCCACACCCTCAGCCCACCCACTTACCTTA 540
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Qy        541 TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAG 600
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Qy        721 GGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAACAAAGGAGAAAGTCCTGTGGA 780
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Db        721 GGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAACAAAGGAGAAAGTCCTGTGGA 780

Qy        781 GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAGCACCATCCCCAT 840
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Db        781 GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAGCACCATCCCCAT 840

Qy        841 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGTAG 900
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Db        841 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGTAG 900

Qy        901 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 960
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Qy        961 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020
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Db        961 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020

Qy       1021 GAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGTGGAGAGTGGGAA 1080
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Qy       1141 ACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGACAGATGACC 1200
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RESULT 8
ABQ80112
ID   ABQ80112 standard; cDNA; 1204 BP.
XX
AC   ABQ80112;
XX
DT   13-JUN-2003  (first entry)
```

XX
DE Modumet coding sequence.
XX
KW Gene; human; Modumet; tumour necrosis factor receptor; super family;
KW type I transmembrane protein; metabolism; body mass; weight loss;
KW obesity; hyperlipidaemia; atherosclerosis; heart disease; stroke;
KW insulin-resistant diabetes; hypertension; cachexia; AIDS-related;
KW cancer-related; weight loss; chronic inflammatory disease-related;
KW anorexia; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 101. .883
FT /*tag= a
FT /product= "Modumet"
XX
PN WO2003009862-A1.
XX
PD 06-FEB-2003.
XX
PF 18-JUL-2002; 2002WO-IB003339.
XX
PR 20-JUL-2001; 2001US-0306745P.
XX
PA (GEST) GENSET SA.
XX
PI Lucas J, Dialynas D, Briggs K;
XX
DR WPI; 2003-229625/22.
DR P-PSDB; AAG79988.
XX
PT Screening for agonist or antagonist of Modumet activity, useful for
PT preventing or treating obesity-related diseases, comprises contacting
PT Modumet polypeptide with a test compound and determining extent of
PT polypeptide binding.
XX
PS Disclosure; Page 32-33; 38pp; English.
XX
CC This sequence encodes human Modumet. Modumet was used in the method of
CC the invention for screening for an agonist or antagonist of Modumet
CC activity. The method comprises contacting Modumet polypeptide with a test
CC compound, determining the extent of binding of the test compound to the
CC polypeptide, and determining whether the test compounds are agonists or
CC antagonists of the Modumet polypeptide. Modumet is a member of the tumour
CC necrosis factor receptor super family, and is a type I transmembrane
CC protein. The method is useful in metabolic research, particularly, in
CC discovering compounds that modulate Modumet activity or that reduce or
CC increase body mass and maintain weight loss, and in preventing or
CC treating obesity-related diseases or disorders such as hyperlipidaemia,
CC atherosclerosis, heart disease, stroke, insulin- resistant diabetes or
CC hypertension, or for preventing or treating disorders associated with
CC excessive weight loss, such as cachexia, cancer-related weight loss, AIDS
CC -related weight loss, chronic inflammatory disease-related weight loss,
CC or anorexia
XX
SQ Sequence 1204 BP; 263 A; 376 C; 338 G; 227 T; 0 U; 0 Other;

Query Match 98.5%; Score 1182.6; DB 8; Length 1204;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1196; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

```
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Qy        181 CCCAGAGAGGCACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240
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Qy        241 ATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 300

Qy        301 GGGGGTCTCCTTCTCTCCTGACCACCACACCCGGCCCCACTGTGAGAGCTGTCGGCACTG 360
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Qy        361 TAACTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCCTGTCG 420
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Db        361 TAACTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCCTGTCG 420

Qy        421 CAATGGCTGGCAGTGCAGGGACAAGGAGTGCACCGAGTGTGATCCTCTTCCAAACCCTTC 480
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Db        781 GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAGCACCATCCCCAT 840

Qy        841 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGTAG 900
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Db        841 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGTAG 900

Qy        901 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 960
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Db        901 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 960

Qy        961 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020
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Db        961 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020

Qy       1021 GAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGTGGAGAGTGGGAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGTGGAGAGTGGGAA 1080

Qy       1081 GCAGGAGCCCAGCCAGCTGCGCGCGCG-TGCAGGAGGGCGGGGGCTCTGGTTGTAAGGCA 1139
              ||||||||||||||||||||||  ||| ||||||||||||||||||||||||  ||
Db       1081 GCAGGAGCCCAGCCAGCTGCGCCTGCGCTGCAGGAGGGCGGGGGCTCTGGTTGTAAAACA 1140

Qy       1140 CACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGACAGATGAC 1199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGACAGATGAC 1200

Qy       1200 C 1200
              |
Db       1201 C 1201
```

```
RESULT 9
ACA64893
ID   ACA64893 standard; DNA; 1204 BP.
XX
AC   ACA64893;
XX
DT   27-JUN-2003  (first entry)
XX
DE   Human CD27 DNA corresponding to M63928.
XX
KW   Human; chronic inflammatory joint disease; infection; tumour;
KW   antiinflammatory; cytostatic; antiarthritic; antirheumatic;
KW   immunosuppressive; gene therapy; etiological pathogenicity; ds.
XX
OS   Homo sapiens.
XX
PN   DE10127572-A1.
XX
PD   05-DEC-2002.
XX
PF   30-MAY-2001; 2001DE-01027572.
XX
PR   30-MAY-2001; 2001DE-01027572.
XX
PA   (PATH-) PATHOARRAY GMBH.
XX
PI   Haeupl T,  Ungethuem U,  Blaess S;
XX
DR   WPI; 2003-240797/24.
XX
PT   Reagents for diagnosis, study and therapy of chronic inflammatory joint
PT   and other diseases, comprises any of many specified genes or derived
PT   proteins.
XX
PS   Claim 1; Page; 12pp; German.
XX
CC   This invention describes a novel reagent for diagnosis, molecular
CC   definition and therapy of chronic inflammatory joint diseases, and other
CC   inflammatory disorders, infective or tumour diseases in humans. The
CC   products of the invention have antiinflammatory, cytostatic,
CC   antiarthritic, antirheumatic and immunosuppressive activity and can be
CC   used for gene therapy. The reagent of the invention and any proteins and
CC   antibodies derived from it, are used (i) for analysing tissue and blood
CC   samples for medical diagnosis; (ii) for diagnosis and characterisation of
CC   chronic joint diseases, on the basis of molecular characterisation, and
CC   determining the etiological pathogenicity principle of as yet
CC   uncharacterised inflammatory diseases, also monitoring progression and/or
CC   treatment of disease, and optimisation of therapy and (iii) for
CC   developing treatments for inflammatory diseases, particularly of joints,
CC   infections and tumours. ACA64801-ACA64965 represent human polynucleotides
CC   used in the method of the invention
XX
SQ   Sequence 1204 BP; 263 A; 376 C; 338 G; 227 T; 0 U; 0 Other;

  Query Match             98.5%;  Score 1182.6;  DB 8;  Length 1204;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 1196;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          1 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60

Qy         61 CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTG 120

Qy        121 GTGGCTGTGCGTTCTGGGGACCCTGGTGGGGCTCTCAGCTACTCCAGCCCCCAAGAGCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGGCTGTGCGTTCTGGGGACCCTGGTGGGGCTCTCAGCTACTCCAGCCCCCAAGAGCTG 180

Qy        181 CCCAGAGAGGCACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCCAGAGAGGCACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240

Qy        241 ATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 300

Qy        301 GGGGGTCTCCTTCTCTCCTGACCACCACACCCGGCCCCACTGTGAGAGCTGTCGGCACTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGGGGTCTCCTTCTCTCCTGACCACCACACCCGGCCCCACTGTGAGAGCTGTCGGCACTG 360

Qy        361 TAACTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCCTGTCG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TAACTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCCTGTCG 420

Qy        421 CAATGGCTGGCAGTGCAGGGACAAGGAGTGCACCGAGTGTGATCCTCTTCCAAACCCTTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGCTGGCAGTGCAGGGACAAGGAGTGCACCGAGTGTGATCCTCTTCCAAACCCTTC 480

Qy        481 GCTGACCGCTCGGTCGTCTCAGGCCCTGAGCCCACACCCTCAGCCCACCCACTTACCTTA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCTGACCGCTCGGTCGTCTCAGGCCCTGAGCCCACACCCTCAGCCCACCCACTTACCTTA 540

Qy        541 TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAG 600

Qy        601 GCAGCTGCCTGCCCGGACTCTCTCTACCCACTGGCCACCCCAAAGATCCCTGTGCAGCTC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCAGCTGCCTGCCCGGACTCTCTCTACCCACTGGCCACCCCAAAGATCCCTGTGCAGCTC 660

Qy        661 CGATTTTATTCGCATCCTTGTGATCTTCTCTGGAATGTTCCTTGTTTTCACCCTGGCCGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGATTTTATTCGCATCCTTGTGATCTTCTCTGGAATGTTCCTTGTTTTCACCCTGGCCGG 720

Qy        721 GGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAACAAAGGAGAAAGTCCTGTGGA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAACAAAGGAGAAAGTCCTGTGGA 780

Qy        781 GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAGCACCATCCCCAT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAGCACCATCCCCAT 840

Qy        841 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGTAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGTAG 900

Qy        901 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 960

Qy        961 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020

Qy       1021 GAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGTGGAGAGTGGGAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGTGGAGAGTGGGAA 1080

Qy       1081 GCAGGAGCCCAGCCAGCTGCGCGCGCG-TGCAGGAGGGCGGGGGCTCTGGTTGTAAGGCA 1139
              |||||||||||||||||||  ||| ||||||||||||||||||||||||  ||
Db       1081 GCAGGAGCCCAGCCAGCTGCGCCTGCGCTGCAGGAGGGCGGGGGCTCTGGTTGTAAAACA 1140

Qy       1140 CACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGACAGATGAC 1199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGACAGATGAC 1200

Qy       1200 C 1200
              |
Db       1201 C 1201


RESULT 10
ADD25535
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ID   ADD25535 standard; DNA; 1204 BP.
XX
AC   ADD25535;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Binding domain-immunoglobulin fusion protein-associated DNA #52.
XX
KW   ds; Binding domain; immunoglobulin; fusion protein; cytostatic;
KW   antiarthritic; immunosuppressive; antidiabetic; antithyroid;
KW   neuroprotective; hinge region; immunoglobulin heavy chain;
KW   CH2 constant region; CH3 constant region; IgG1;
KW   antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW   malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
KW   rheumatoid arthritis; myasthenia gravis; Grave's disease;
KW   type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX
OS   Unidentified.
XX
PN   US2003118592-A1.
XX
PD   26-JUN-2003.
XX
PF   25-JUL-2002; 2002US-00207655.
XX
PR   17-JAN-2001; 2001US-0367358P.
PR   17-JAN-2002; 2002US-00053530.
PR   03-JUN-2002; 2002US-0385691P.
XX
PA   (GENE-) GENECRAFT INC.
XX
PI   Ledbetter JA,  Hayden-Ledbetter MS,  Thompson PA;
XX
DR   WPI; 2003-801317/75.
XX
PT   New binding domain-immunoglobulin fusion protein, useful for treating a
PT   subject having or suspected of having a malignant condition or a B-cell
PT   disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX
PS   Disclosure; SEQ ID NO 96; 157pp; English.
XX
CC   Unidentified
XX
SQ   Sequence 1204 BP; 263 A; 376 C; 338 G; 227 T; 0 U; 0 Other;

  Query Match           98.5%;  Score 1182.6;  DB 10;  Length 1204;
  Best Local Similarity  99.6%;  Pred. No. 0;
  Matches 1196;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          1 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60

Qy         61 CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTG 120

Qy        121 GTGGCTGTGCGTTCTGGGGACCCTGGTGGGGCTCTCAGCTACTCCAGCCCCCAAGAGCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGGCTGTGCGTTCTGGGGACCCTGGTGGGGCTCTCAGCTACTCCAGCCCCCAAGAGCTG 180

Qy        181 CCCAGAGAGGCACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCCAGAGAGGCACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240

Qy        241 ATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 300

Qy        301 GGGGGTCTCCTTCTCTCCTGACCACCACACCCGGCCCCACTGTGAGAGCTGTCGGCACTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGGGGTCTCCTTCTCTCCTGACCACCACACCCGGCCCCACTGTGAGAGCTGTCGGCACTG 360

Qy        361 TAACTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCCTGTCG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TAACTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCCTGTCG 420

Qy        421 CAATGGCTGGCAGTGCAGGGACAAGGAGTGCACCGAGTGTGATCCTCTTCCAAACCCTTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGCTGGCAGTGCAGGGACAAGGAGTGCACCGAGTGTGATCCTCTTCCAAACCCTTC 480

Qy        481 GCTGACCGCTCGGTCGTCTCAGGCCCTGAGCCCACACCCTCAGCCCACCCACTTACCTTA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCTGACCGCTCGGTCGTCTCAGGCCCTGAGCCCACACCCTCAGCCCACCCACTTACCTTA 540

Qy        541 TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAG 600

Qy        601 GCAGCTGCCTGCCCGGACTCTCTCTACCCACTGGCCACCCCAAAGATCCCTGTGCAGCTC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCAGCTGCCTGCCCGGACTCTCTCTACCCACTGGCCACCCCAAAGATCCCTGTGCAGCTC 660

Qy        661 CGATTTTATTCGCATCCTTGTGATCTTCTCTGGAATGTTCCTTGTTTTCACCCTGGCCGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGATTTTATTCGCATCCTTGTGATCTTCTCTGGAATGTTCCTTGTTTTCACCCTGGCCGG 720

Qy        721 GGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAACAAAGGAGAAAGTCCTGTGGA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAACAAAGGAGAAAGTCCTGTGGA 780

Qy        781 GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAGCACCATCCCCAT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAGCACCATCCCCAT 840

Qy        841 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGTAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGTAG 900

Qy        901 CTGCACTACAGCCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 960

Qy        961 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020

Qy       1021 GAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGTGGAGAGTGGGAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGTGGAGAGTGGGAA 1080

Qy       1081 GCAGGAGCCCAGCCAGCTGCGCGCGCG-TGCAGGAGGGCGGGGGCTCTGGTTGTAAGGCA 1139
              |||||||||||||||||||||||||||  ||| |||||||||||||||||||||||||  ||
Db       1081 GCAGGAGCCCAGCCAGCTGCGCCTGCGCTGCAGGAGGGCGGGGGCTCTGGTTGTAAAACA 1140

Qy       1140 CACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGACAGATGAC 1199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGACAGATGAC 1200

Qy       1200 C 1200
              |
Db       1201 C 1201
```

```
RESULT 11
ADL15014
ID   ADL15014 standard; DNA; 1204 BP.
XX
AC   ADL15014;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human T-cell activation protein DNA for cancer treatment.
XX
KW   ds; gene; cytostatic; gene therapy; binding moiety; medicine; imaging;
KW   diagnosis; prognosis; mantle cell lymphoma; cancer.
```

```
XX
OS   Homo sapiens.
XX
PN   WO2003068268-A2.
XX
PD   21-AUG-2003.
XX
PF   13-FEB-2003; 2003WO-EP001461.
XX
PR   14-FEB-2002; 2002GB-00003480.
PR   29-JUN-2002; 2002GB-00015095.
XX
PA   (BIOI-) BIOINVENT INT AB.
XX
PI   Ek S,  Borrebaeck CAK,  Ehinger M;
XX
DR   WPI; 2003-697496/66.
DR   P-PSDB; ADL15013.
XX
PT   New compound for treating, imaging, diagnosing or prognosing mantle cell
PT   lymphoma, comprises a binding moiety (e.g. antibody) that binds to a
PT   protein (e.g. human autotaxin polypeptide), and a further moiety (e.g.
PT   nucleic acid).
XX
PS   Disclosure; SEQ ID NO 26; 342pp; English.
XX
CC   The invention relates to a compound comprising a binding moiety which
CC   selectively binds to a protein or polypeptide listed in the specification
CC   (e.g. human autotaxin polypeptide or human CD24 signal transducer
CC   polypeptide), and a further moiety. The compound is useful in medicine or
CC   in the treatment, imaging, diagnosis or prognosis of mantle cell
CC   lymphomas (MCL). It is used in preparing a medicament for treating MCL, a
CC   diagnostic or prognostic agent for MCL, or an agent for imaging MCL cells
CC   in the body of an individual. This sequence corresponds to a gene
CC   encoding one of the polypeptides of the invention.
XX
SQ   Sequence 1204 BP; 263 A; 376 C; 338 G; 227 T; 0 U; 0 Other;

  Query Match             98.5%;  Score 1182.6;  DB 10;  Length 1204;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 1196;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          1 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60

Qy         61 CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTG 120

Qy        121 GTGGCTGTGCGTTCTGGGGACCCTGGTGGGGCTCTCAGCTACTCCAGCCCCCAAGAGCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGGCTGTGCGTTCTGGGGACCCTGGTGGGGCTCTCAGCTACTCCAGCCCCCAAGAGCTG 180

Qy        181 CCCAGAGAGGCACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCCAGAGAGGCACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240

Qy        241 ATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 300

Qy        301 GGGGGTCTCCTTCTCTCCTGACCACCACACCCGGCCCCACTGTGAGAGCTGTCGGCACTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGGGGTCTCCTTCTCTCCTGACCACCACACCCGGCCCCACTGTGAGAGCTGTCGGCACTG 360

Qy        361 TAACTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCCTGTCG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TAACTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCCTGTCG 420

Qy        421 CAATGGCTGGCAGTGCAGGGACAAGGAGTGCACCGAGTGTGATCCTCTTCCAAACCCTTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGCTGGCAGTGCAGGGACAAGGAGTGCACCGAGTGTGATCCTCTTCCAAACCCTTC 480

Qy        481 GCTGACCGCTCGGTCGTCTCAGGCCCTGAGCCCACACCCTCAGCCCACCCACTTACCTTA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCTGACCGCTCGGTCGTCTCAGGCCCTGAGCCCACACCCTCAGCCCACCCACTTACCTTA 540

Qy        541 TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAG 600

Qy        601 GCAGCTGCCTGCCCGGACTCTCTCTACCCACTGGCCACCCCAAAGATCCCTGTGCAGCTC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCAGCTGCCTGCCCGGACTCTCTCTACCCACTGGCCACCCCAAAGATCCCTGTGCAGCTC 660

Qy        661 CGATTTTATTCGCATCCTTGTGATCTTCTCTGGAATGTTCCTTGTTTTCACCCTGGCCGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGATTTTATTCGCATCCTTGTGATCTTCTCTGGAATGTTCCTTGTTTTCACCCTGGCCGG 720

Qy        721 GGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAACAAAGGAGAAAGTCCTGTGGA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAACAAAGGAGAAAGTCCTGTGGA 780

Qy        781 GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAGCACCATCCCCAT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAGCACCATCCCCAT 840

Qy        841 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGTAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGTAG 900

Qy        901 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 960

Qy        961 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020

Qy       1021 GAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGTGGAGAGTGGGAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGTGGAGAGTGGGAA 1080

Qy       1081 GCAGGAGCCCAGCCAGCTGCGCGCGCG-TGCAGGAGGGCGGGGGCTCTGGTTGTAAGGCA 1139
              |||||||||||||||||||  ||| |||||||||||||||||||||||||  ||
Db       1081 GCAGGAGCCCAGCCAGCTGCGCCTGCGCTGCAGGAGGGCGGGGGCTCTGGTTGTAAAACA 1140

Qy       1140 CACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGACAGATGAC 1199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGACAGATGAC 1200

Qy       1200 C 1200
              |
Db       1201 C 1201


RESULT 12
ADI31701
ID   ADI31701 standard; cDNA; 1204 BP.
XX
AC   ADI31701;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Human cDNA #1027.
XX
KW   Human; gene; ss; immunological response; immunopathological condition;
KW   Crohn's disease; asthma; ulcerative colitis; hypereosinophilia;
KW   irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
KW   acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer;
KW   osteopathic; antiarthritic; antirheumatic; cytostatic.
XX
OS   Homo sapiens.
XX
PN   US6607879-B1.
```

XX
PD 19-AUG-2003.
XX
PF 09-FEB-1998; 98US-00023655.
XX
PR 09-FEB-1998; 98US-00023655.
XX
PA (INCY-) INCYTE CORP.
XX
PI Cocks BG, Stuart SG, Seilhamer JJ;
XX
DR WPI; 2003-895307/82.
XX
PT A composition comprising a plurality of cDNAs, useful for detecting
PT altered expression of genes in an immunological response or for
PT diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
PT or osteoarthritis.
XX
PS Claim 1; SEQ ID NO 1027; 50pp; English.
XX
CC The invention relates to a composition comprising a plurality of cDNAs
CC for detecting the altered expression of genes in an immunological
CC response. The invention also relates to a method of diagnosing or
CC monitoring the treatment of an immunopathological condition in a sample,
CC comprising obtaining nucleic acids from a sample, contacting the nucleic
CC acids of the sample with an array comprising the plurality of cDNAs under
CC conditions to form one or more hybridisation complexes, detecting the
CC hybridisation complexes and comparing the levels of the detected
CC hybridisation complexes with the level of hybridisation complexes
CC detected in a non-diseased sample, where an altered level of the detected
CC hybridisation complexes correlates with the presence of an
CC immunopathological condition. Also disclosed are an expression profile
CC comprising a microarray and a plurality of detectable complexes and a
CC method for identifying a plurality of polynucleotide probes. The cDNAs
CC are useful as hybridisable array elements in a microarray for monitoring
CC the expression of target polynucleotides. The microarray can be used in
CC the diagnosis of an immunopathology, such as Crohn's disease, asthma,
CC ulcerative colitis, hypereosinophilia, irritable bowel syndrome,
CC osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in
CC identifying agents for the treatment of the diseases. The microarray may
CC also be used in drug discovery and development, toxicological and
CC carcinogenicity studies, forensics or pharmacogenomics. The composition
CC may also be used in purification of a subpopulation of mRNAs, cDNAs or
CC genomic fragments. This sequence represents a human cDNA of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification but was obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 1204 BP; 263 A; 376 C; 338 G; 227 T; 0 U; 0 Other;

Query Match 98.5%; Score 1182.6; DB 11; Length 1204;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1196; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

```
Qy          1 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60

Qy         61 CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTG 120

Qy        121 GTGGCTGTGCGTTCTGGGGACCCTGGTGGGGCTCTCAGCTACTCCAGCCCCCAAGAGCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGGCTGTGCGTTCTGGGGACCCTGGTGGGGCTCTCAGCTACTCCAGCCCCCAAGAGCTG 180

Qy        181 CCCAGAGAGGCACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCCAGAGAGGCACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240

Qy        241 ATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 300

Qy        301 GGGGGTCTCCTTCTCTCCTGACCACCACACCCGGCCCCACTGTGAGAGCTGTCGGCACTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGGGGTCTCCTTCTCTCCTGACCACCACACCCGGCCCCACTGTGAGAGCTGTCGGCACTG 360

Qy        361 TAACTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCCTGTCG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TAACTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCCTGTCG 420

Qy        421 CAATGGCTGGCAGTGCAGGGACAAGGAGTGCACCGAGTGTGATCCTCTTCCAAACCCTTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGCTGGCAGTGCAGGGACAAGGAGTGCACCGAGTGTGATCCTCTTCCAAACCCTTC 480

Qy        481 GCTGACCGCTCGGTCGTCTCAGGCCCTGAGCCCACACCCTCAGCCCACCCACTTACCTTA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCTGACCGCTCGGTCGTCTCAGGCCCTGAGCCCACACCCTCAGCCCACCCACTTACCTTA 540

Qy        541 TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAG 600

Qy        601 GCAGCTGCCTGCCCGGACTCTCTCTACCCACTGGCCACCCCAAAGATCCCTGTGCAGCTC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCAGCTGCCTGCCCGGACTCTCTCTACCCACTGGCCACCCCAAAGATCCCTGTGCAGCTC 660

Qy        661 CGATTTTATTCGCATCCTTGTGATCTTCTCTGGAATGTTCCTTGTTTTCACCCTGGCCGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGATTTTATTCGCATCCTTGTGATCTTCTCTGGAATGTTCCTTGTTTTCACCCTGGCCGG 720

Qy        721 GGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAACAAAGGAGAAAGTCCTGTGGA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAACAAAGGAGAAAGTCCTGTGGA 780

Qy        781 GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAGCACCATCCCCAT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAGCACCATCCCCAT 840

Qy        841 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGTAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGTAG 900

Qy        901 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 960

Qy        961 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020

Qy       1021 GAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGTGGAGAGTGGGAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGTGGAGAGTGGGAA 1080

Qy       1081 GCAGGAGCCCAGCCAGCTGCGCGCGCG-TGCAGGAGGGCGGGGGCTCTGGTTGTAAGGCA 1139
              |||||||||||||||||||  ||| |||||||||||||||||||||||||  ||
Db       1081 GCAGGAGCCCAGCCAGCTGCGCCTGCGCTGCAGGAGGGCGGGGGCTCTGGTTGTAAAACA 1140

Qy       1140 CACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGACAGATGAC 1199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGACAGATGAC 1200

Qy       1200 C 1200
              |
Db       1201 C 1201
```

RESULT 13
ADQ19552
ID ADQ19552 standard; DNA; 1204 BP.
XX
AC ADQ19552;
XX
DT 26-AUG-2004 (first entry)

```
XX
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 2371.
XX
KW   soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
KW   ds.
XX
OS   Homo sapiens.
XX
PN   WO2004048938-A2.
XX
PD   10-JUN-2004.
XX
PF   26-NOV-2003; 2003WO-US038193.
XX
PR   26-NOV-2002; 2002US-0429739P.
XX
PA   (PROT-) PROTEIN DESIGN LABS INC.
XX
PI   Aziz N,  Ginsburg WM,  Zlotnik A;
XX
DR   WPI; 2004-441208/41.
XX
PT   Early detection of soft tissue sarcoma comprises determining expression
PT   of a gene in a first soft tissue sample and a normal soft tissue sample
PT   and comparing the gene expression, also useful in treating soft tissue
PT   sarcoma.
XX
PS   Example 2; SEQ ID NO 2371; 210pp; English.
XX
CC   The invention relates to a novel method for detecting soft tissue sarcoma
CC   which comprises obtaining a first soft tissue sample from an individual
CC   and a normal soft tissue sample from the same or different individual,
CC   determining the expression of a gene in both samples and comparing the
CC   expression of the gene in both soft tissue samples, where a higher level
CC   of protein expression in the first soft tissue sample indicates the
CC   presence of soft tissue sarcoma. The method of the invention has
CC   cytostatic applications and may be useful for detecting soft tissue
CC   sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC   acid sequences may be useful in diagnostic and screening applications.
CC   The current sequence is that of a human soft tissue sarcoma-upregulated
CC   DNA of the invention. The current sequence is not shown within the
CC   specification per se but was submitted in CD format by the inventor.
XX
SQ   Sequence 1204 BP; 263 A; 376 C; 338 G; 227 T; 0 U; 0 Other;

  Query Match            98.5%;  Score 1182.6;  DB 12;  Length 1204;
  Best Local Similarity  99.6%;  Pred. No. 0;
  Matches 1196;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          1 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60

Qy         61 CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTG 120

Qy        121 GTGGCTGTGCGTTCTGGGGACCCTGGTGGGGCTCTCAGCTACTCCAGCCCCCAAGAGCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGGCTGTGCGTTCTGGGGACCCTGGTGGGGCTCTCAGCTACTCCAGCCCCCAAGAGCTG 180

Qy        181 CCCAGAGAGGCACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCCAGAGAGGCACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240

Qy        241 ATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 300

Qy        301 GGGGGTCTCCTTCTCTCCTGACCACCACACCCGGCCCCACTGTGAGAGCTGTCGGCACTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGGGGTCTCCTTCTCTCCTGACCACCACACCCGGCCCCACTGTGAGAGCTGTCGGCACTG 360

Qy        361 TAACTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCCTGTCG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TAACTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCCTGTCG 420

Qy        421 CAATGGCTGGCAGTGCAGGGACAAGGAGTGCACCGAGTGTGATCCTCTTCCAAACCCTTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGCTGGCAGTGCAGGGACAAGGAGTGCACCGAGTGTGATCCTCTTCCAAACCCTTC 480

Qy        481 GCTGACCGCTCGGTCGTCTCAGGCCCTGAGCCCACACCCTCAGCCCACCCACTTACCTTA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCTGACCGCTCGGTCGTCTCAGGCCCTGAGCCCACACCCTCAGCCCACCCACTTACCTTA 540

Qy        541 TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAG 600

Qy        601 GCAGCTGCCTGCCCGGACTCTCTCTACCCACTGGCCACCCCAAAGATCCCTGTGCAGCTC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCAGCTGCCTGCCCGGACTCTCTCTACCCACTGGCCACCCCAAAGATCCCTGTGCAGCTC 660

Qy        661 CGATTTTATTCGCATCCTTGTGATCTTCTCTGGAATGTTCCTTGTTTTCACCCTGGCCGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGATTTTATTCGCATCCTTGTGATCTTCTCTGGAATGTTCCTTGTTTTCACCCTGGCCGG 720

Qy        721 GGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAACAAAGGAGAAAGTCCTGTGGA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAACAAAGGAGAAAGTCCTGTGGA 780

Qy        781 GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAGCACCATCCCCAT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAGCACCATCCCCAT 840

Qy        841 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGTAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGTAG 900

Qy        901 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 960

Qy        961 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020

Qy       1021 GAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGTGGAGAGTGGGAA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGTGGAGAGTGGGAA 1080

Qy       1081 GCAGGAGCCCAGCCAGCTGCGCGCGCG-TGCAGGAGGGCGGGGGCTCTGGTTGTAAGGCA 1139
              |||||||||||||||||||||||||||  ||| |||||||||||||||||||||||||  ||
Db       1081 GCAGGAGCCCAGCCAGCTGCGCCTGCGCTGCAGGAGGGCGGGGGCTCTGGTTGTAAAACA 1140

Qy       1140 CACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGACAGATGAC 1199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGACAGATGAC 1200

Qy       1200 C 1200
              |
Db       1201 C 1201


RESULT 14
ADS83768
ID   ADS83768 standard; cDNA; 1204 BP.
XX
AC   ADS83768;
XX
DT   11-AUG-2005  (first entry)
XX
DE   Human lymph node cDNA #1027.
XX
KW   ss; gene; human; immunological response; blood cell; cancer;
KW   immunopathological; AIDS; allergy; anaemia; asthma; atherosclerosis;
```

```
KW   bronchitis; ulcerative colitis; diabetes; multiple sclerosis;
KW   osteoporosis; pancreatitis; infection; arthritis; lymph node.
XX
OS   Homo sapiens.
XX
PN   US2004077003-A1.
XX
PD   22-APR-2004.
XX
PF   14-AUG-2003; 2003US-00641643.
XX
PR   09-FEB-1998;   98US-00023655.
XX
PA   (INCY-) INCYTE CORP.
XX
PI   Cocks BG,  Stuart SG,  Seilhamer JJ;
XX
DR   WPI; 2004-387937/36.
XX
PT   New compositions having a number of first, second and third
PT   polynucleotide probes, useful in research and diagnostic applications in
PT   cancer and immunological conditions e.g. AIDS, diabetes, osteoporosis and
PT   infections.
XX
PS   Claim 15; SEQ ID NO 1027; 16pp; English.
XX
CC   The invention relates to polynucleotides which are used as probes to
CC   detect genes differentially expressed in an immunological response,
CC   abundantly expressed in an immunological response and/or coding for a
CC   polypeptide known to regulate blood cell biology. The polynucleotides are
CC   useful in research and diagnostic applications particularly in cancer and
CC   immunopathological conditions, such as AIDS, allergies, anaemia, asthma,
CC   atherosclerosis, bronchitis, ulcerative colitis, diabetes, multiple
CC   sclerosis, osteoporosis, pancreatitis, infections and arthritis. The
CC   present sequence represents a human lymph node cDNA used to detect blood
CC   cell and immunological response gene expression. Note: The present
CC   sequence does not appear in the printed specification but was obtained in
CC   electronic format from the USPTO web site
CC   (seqdata.uspto.gov/sequence.html?DocID=20040077003).
XX
SQ   Sequence 1204 BP; 263 A; 376 C; 338 G; 227 T; 0 U; 0 Other;

  Query Match           98.5%;  Score 1182.6;  DB 13;  Length 1204;
  Best Local Similarity 99.6%;  Pred. No. 0;
  Matches 1196;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          1 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60

Qy         61 CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTG 120

Qy        121 GTGGCTGTGCGTTCTGGGGACCCTGGTGGGGCTCTCAGCTACTCCAGCCCCCAAGAGCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGGCTGTGCGTTCTGGGGACCCTGGTGGGGCTCTCAGCTACTCCAGCCCCCAAGAGCTG 180

Qy        181 CCCAGAGAGGCACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCCAGAGAGGCACTACTGGGCTCAGGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGAAC 240

Qy        241 ATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 300

Qy        301 GGGGGTCTCCTTCTCTCCTGACCACCACACCCGGCCCCACTGTGAGAGCTGTCGGCACTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGGGGTCTCCTTCTCTCCTGACCACCACACCCGGCCCCACTGTGAGAGCTGTCGGCACTG 360

Qy        361 TAACTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCCTGTCG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TAACTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCCTGTCG 420

Qy        421 CAATGGCTGGCAGTGCAGGGACAAGGAGTGCACCGAGTGTGATCCTCTTCCAAACCCTTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGCTGGCAGTGCAGGGACAAGGAGTGCACCGAGTGTGATCCTCTTCCAAACCCTTC 480

Qy        481 GCTGACCGCTCGGTCGTCTCAGGCCCTGAGCCCACACCCTCAGCCCACCCACTTACCTTA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCTGACCGCTCGGTCGTCTCAGGCCCTGAGCCCACACCCTCAGCCCACCCACTTACCTTA 540

Qy        541 TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAG 600

Qy        601 GCAGCTGCCTGCCCGGACTCTCTCTACCCACTGGCCACCCCAAAGATCCCTGTGCAGCTC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCAGCTGCCTGCCCGGACTCTCTCTACCCACTGGCCACCCCAAAGATCCCTGTGCAGCTC 660

Qy        661 CGATTTTATTCGCATCCTTGTGATCTTCTCTGGAATGTTCCTTGTTTTCACCCTGGCCGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGATTTTATTCGCATCCTTGTGATCTTCTCTGGAATGTTCCTTGTTTTCACCCTGGCCGG 720

Qy        721 GGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAACAAAGGAGAAAGTCCTGTGGA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GGCCCTGTTCCTCCATCAACGAAGGAAATATAGATCAAACAAAGGAGAAAGTCCTGTGGA 780

Qy        781 GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAGCACCATCCCCAT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAGCACCATCCCCAT 840

Qy        841 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGTAG 900
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Qy        901 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 960
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Qy        961 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020
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Db        961 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020

Qy       1021 GAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGTGGAGAGTGGGAA 1080
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Db       1021 GAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGTGGAGAGTGGGAA 1080

Qy       1081 GCAGGAGCCCAGCCAGCTGCGCGCGCG-TGCAGGAGGGCGGGGGCTCTGGTTGTAAGGCA 1139
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Qy       1140 CACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGACAGATGAC 1199
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Db       1141 CACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGACAGATGAC 1200

Qy       1200 C 1200
              |
Db       1201 C 1201


RESULT 15
ADQ23741
ID   ADQ23741 standard; DNA; 1711 BP.
XX
AC   ADQ23741;
XX
DT   26-AUG-2004  (first entry)
XX
DE   Human soft tissue sarcoma-upregulated DNA - SEQ ID 6561.
XX
KW   soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
KW   ds.
XX
OS   Homo sapiens.
XX
```

PN WO2004048938-A2.
XX
PD 10-JUN-2004.
XX
PF 26-NOV-2003; 2003WO-US038193.
XX
PR 26-NOV-2002; 2002US-0429739P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Aziz N, Ginsburg WM, Zlotnik A;
XX
DR WPI; 2004-441208/41.
XX
PT Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.
XX
PS Example 2; SEQ ID NO 6561; 210pp; English.
XX
CC The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC DNA of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
XX
SQ Sequence 1711 BP; 441 A; 524 C; 472 G; 274 T; 0 U; 0 Other;

Query Match 98.5%; Score 1182.6; DB 12; Length 1711;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1196; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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Qy          1 GGGGTGCAAAGAAGAGACAGCAGCGCCCAGCTTGGAGGTGCTAACTCCAGAGGCCAGCAT 60
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Qy         61 CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTG 120
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Db        158 CAGCAACTGGGCACAGAAAGGAGCCGCCTGGGCAGGGACCATGGCACGGCCACATCCCTG 217

Qy        121 GTGGCTGTGCGTTCTGGGGACCCTGGTGGGGCTCTCAGCTACTCCAGCCCCCAAGAGCTG 180
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Db        218 GTGGCTGTGCGTTCTGGGGACCCTGGTGGGGCTCTCAGCTACTCCAGCCCCCAAGAGCTG 277

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Qy        241 ATTCCTCGTGAAGGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGCATACC 300
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Db        398 GGGGGTCTCCTTCTCTCCTGACCACCACACCCGGCCCCACTGTGAGAGCTGTCGGCACTG 457

Qy        361 TAACTCTGGTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCCTGTCG 420
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Qy        421 CAATGGCTGGCAGTGCAGGGACAAGGAGTGCACCGAGTGTGATCCTCTTCCAAACCCTTC 480
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Qy        541 TGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAG 600
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Qy        601 GCAGCTGCCTGCCCGGACTCTCTCTACCCACTGGCCACCCCAAAGATCCCTGTGCAGCTC 660
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Qy        661 CGATTTTATTCGCATCCTTGTGATCTTCTCTGGAATGTTCCTTGTTTTCACCCTGGCCGG 720
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Qy        781 GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAGCACCATCCCCAT 840
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Db        878 GCCTGCAGAGCCTTGTCGTTACAGCTGCCCCAGGGAGGAGGAGGGCAGCACCATCCCCAT 937

Qy        841 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGTAG 900
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Db        938 CCAGGAGGATTACCGAAAACCGGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGTAG 997

Qy        901 CTGCACTACAGCCCTGGCCTCCACCCCCACCCCGCCGACCATCCAAGGGAGAGTGAGACC 960
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Qy        961 TGGCAGCCACAACTGCAGTCCCATCCTCTTGTCAGGGCCCTTTCCTGTGTACACGTGACA 1020
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Qy       1021 GAGTGCCTTTTCGAGACTGGCAGGGACGAGGACAAATATGGATGAGGTGGAGAGTGGGAA 1080
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Qy       1140 CACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGACAGATGAC 1199
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Db       1238 CACTTCCTGCTGCGAAAGACCCACATGCTACAAGACGGGCAAAATAAAGTGACAGATGAC 1297

Qy       1200 C 1200
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Db       1298 C 1298
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Search completed: December 7, 2005, 04:16:19
Job time : 818 secs